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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:37:33 ; Search time 78.7907 Seconds
(without alignments)
68.722 Million cell updates/sec

Title: US-10-706-275-1
Perfect score: 64
Sequence: 1 ASREAKQVEKALE 14

Scoring table: BL00M62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries
Database : A_Geneseq_16Dec04 : *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2010s: *
5: geneseqp2020s: *
6: geneseqp2030sab: *
7: geneseqp2003bs: *
8: geneseqp2004s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	64	100.0	20	AAR43343	Aar43343 B cell ep
2	64	100.0	20	AAR97390	Aar97390 Streptoco
3	64	100.0	20	AAW69281	AAw69281 Streptoco
4	64	100.0	29	ADK00565	Adk00565 Immunogen
5	64	100.0	45	ADK00571	Adk00571 Immunogen
6	64	100.0	46	ADK00569	Adk00569 Immunogen
7	64	100.0	46	ADK00572	Adk00572 Immunogen
8	64	100.0	47	ADK00570	Adk00570 Immunogen
9	64	100.0	234	ADR10221	Aar10221 Streptoco
10	64	100.0	236	AAB03118	Aab03118 C-terminal
11	64	100.0	254	AAK50228	Aar50228 Sequence
12	64	100.0	281	AAR20128	Aar20128 Sequence
13	64	100.0	284	AAR50229	Aar50229 Sequence
14	64	100.0	305	AAR50996	Aar50996 Recombina
15	64	100.0	305	AAB03117	Aab03117 S. pyogen
16	64	100.0	441	AAP90955	Aap90955 M6 strept
17	64	100.0	441	AAR41780	Aar41780 Streptoco
18	64	100.0	441	ADG62862	Adg62862 Streptoco
19	64	100.0	483	AAW08927	Aaw08927 Type-6 M-
20	64	100.0	484	ABP30015	Abp30015 Streptoco
21	64	100.0	484	ADR83959	Adr83959 S. pyogen
22	64	100.0	539	ADP49327	Adp49327 S pyogen
23	57	89.1	28	AAW04353	Aaw04353 Chimaeric
24	56	87.5	12	AAR97415	Aar97415 Streptoco
25	56	87.5	28	AAW04354	Aaw04354 Chimaeric

ALIGNMENTS

RESULT 1
AAR43343 standard; peptide; 20 AA.
ID XX
XX AAR43343;

AC XX
XX DT 25-MAR-2003 (revised)
DT 21-MAY-1994 (first entry)

XX DE B cell epitope from Streptococcus M protein.
XX Group A beta haemolytic streptococci; antibody; human heart tissue;
KW vaccine; humoral immunity; diagnosis.
XX Synthetic.
OS XX
PN WO9321220-A1.
XX PD 28-OCT-1993.
XX PD 28-OCT-1993.
XX PP 30-MAR-1993; 93WO-AU000131.
XX PR 08-APR-1992; 92AU-00001800.

XX (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX PI Good MF, Praksakorn S;
XX DR WPI; 1993-351655/44.

XX PT Synthetic peptide - comprises at least one B-cell epitope from streptococcal M-protein, useful in vaccine for streptococcal infections.
PT PP 30-MAR-1993; 93WO-AU000131.
XX PS Claim 7; Page 38; 57pp; English.
XX PR 08-APR-1992; 92AU-00001800.

CC The peptide comprises an N-terminal sequence derived from the conserved region of the M protein of group A beta-haemolytic streptococci (residues 337-492 of the type 5 M-protein). The peptide shown, Peptide 145 comprises at least 1 B cell epitope, where an antibody reactive to the peptide is only minimally reactive to human heart tissue. The peptide is useful in a vaccine for inducing humoral immunity against streptococcal infections. Antibodies to the peptide are useful in diagnosis of such infections. (Updated on 25-MAR-2003 to correct PN
CC Field.)
CC Sequence 20 AA;
SQ Sequence 20 AA;

Query Match 100.0%; Score 64; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 Db 7 ASREAKKQVEKALE 20

RESULT 2
 ARR97390 ID ARR97390 standard; peptide; 20 AA.

XX
 AC AAR97390;
 DT 27-AUG-2003 (revised)
 DT 02-DEC-1996 (first entry)
 DB Streptococcal M protein peptide p145, for use in chimaeric peptide
 XX
 KW Streptococcal; M protein; peptide; p145; chimaeric; chimeric; B-cell; conformational epitope; alpha-helix; GCN4; leucine zipper; detection; mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy; diagnosis.
 XX
 OS Streptococcus sp.
 XX
 PN W09611944-A1.
 XX
 PD 25-APR-1996.
 XX
 PF 16-OCT-1995; 95WO-AU000681.
 XX
 PR 14-OCT-1994; 94AU-000008851.
 XX
 PA (COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UWME) UNIV MELBOURNE.
 PA (HALL) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT) BIOCOP AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.

P1 Cooper JA, Relf WA, Good MF, Saul AJ;
 XX
 DR WPI; 1996-221939/22.

PT New chimeric peptide(s) including a conformational epitope - inserted into a peptide having similar native conformation, useful in vaccines and for determin. of minimal epitope(s) or for mapping amphipathic helices.

XX
 P5 Claim 4; Page 80; 99pp; English.

CC The present peptide is the Streptococcal M protein peptide p145 (Prusakorn et al, J. Immunol. 149: 2729-2735 (1992)), used in the construction of a novel chimaeric peptide (CP). The CP comprises a B-cell conformational epitope from within the present peptide, inserted into a 2nd peptide, pref. an alpha-helical coil based on the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar conformation, enabling the epitope to be presented in an immunologically active conformation. The CP can be used in a novel detection/mapping process, e.g. to determine the min. epitope required to induce opsonic antibodies (Ab), and in vaccines against gp. A streptococci Ab raised against the CP can be used for immunotherapy and diagnosis, while the CP can be used diagnostically to detect Ab. (Updated on 27-AUG-2003 to correct OS field.)
 CC
 XX Sequence 20 AA;

CC Query Match 100.0%; Score 64; DB 2; Length 20;
 CC Best Local Similarity 100.0%; Pred. No. 0.0019;
 CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC Qy 1 ASREAKKQVEKALE 14
 CC Db 7 ASREAKKQVEKALE 20

Best Local Similarity 100.0%; Pred. No. 0.0019;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 Db 7 ASREAKKQVEKALE 20

Db 7 ASREAKKQVEKALE 20

RESULT 3
 AAW69281 standard; peptide; 20 AA.

XX
 AC AAW69281;

XX
 DT 29-OCT-1998 (first entry)

XX Streptococcus group A protein fragment.

XX Acryloylated peptide polymer; immune response; peptide epitope;

XX synthetic vaccine; enzymatically cleavable site.

XX Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 1 /note= "linked to acryloylated peptide polymer"

XX FT FT

XX PN W09834968-A1.

XX PD 13-AUG-1998.

XX PP 10-FEB-1998;

XX PR 11-FEB-1997;

XX PR 03-OCT-1997;

XX PR 03-OCT-1997;

XX XX (COUNCIL QUEENSLAND INST MEDICAL RES.

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.

PA (UWME) UNIV MELBOURNE.

PA (HALL) HALL INST MEDICAL RES WALTER & ELIZA.

XX PA (CSLIC-) CSL LTD.

PI Jackson DC, Obrien-Simpson NM, Brown IE, Zeng W, Ede NJ;

PI Brandt ER, Good MF,

XX DR WPI; 1998-447177/38.

XX Acryloylated peptide polymers - useful for synthetic vaccine technology, for raising an immune response to peptide epitope and as diagnostic tool.

XX Example 1; Page 20; 77pp; English.

XX This sequence represents a fragment of a Streptococcus group A protein.

CC This sequence was used to test the acryloylated peptide polymer of the invention. The peptide polymers are used to raise an immune response to a peptide epitope (such as this sequence), and also as diagnostic tools.

CC This sequence was used to prepare with virtually any

CC polymers (molecular wt. >600 kDa.) can be prepared with a method that allows

CC number of the same or different epitopes by a method that allows

CC purification of the individual determinants, avoids errors inherent in

CC long sequential syntheses in which protected peptide fragments are not

CC used, thus avoiding solubility and purification problems. Multiple copies

CC of many different peptide epitopes may be incorporated into a single

CC polymeric structure to allow utilisation of the range of T cell epitopes

CC required for outbred populations in conjunction with epitopes

CC representing different pathogenic serotypes, thus making them a

CC significant advance in synthetic vaccine technology

XX Sequence 20 AA:

XX Query Match 100.0%; Score 64; DB 2; Length 20;

CC Best Local Similarity 100.0%; Pred. No. 0.0019;

CC Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CC Qy 1 ASREAKKQVEKALE 14

CC Db 7 ASREAKKQVEKALE 20

RESULT 4

KW Antinfertility; Vaccine; antibody.
XX OS Synthetic.
XX
ID ADK00565 standard; peptide; 29 AA.
XX AC ADK00565;
XX PN WO2004014956-A1.
XX DT 06-MAY-2004 (first entry)
XX DB Immunogenic lipopeptide of the invention #101.
XX KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
XX Antinfertility; vaccine; antibody.
OS Synthetic.
XX
PN WO2004014956-A1.
XX PD 19-FEB-2004.
XX PF 12-AUG-2003; 2003WO-AU001018.
XX PR 12-AUG-2002; 2002US-0402838P.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2002; 2002US-0402838P.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2003; 2003WO-AU001018.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2002; 2002US-0402838P.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

RESULT 5

KW Antinfertility; Vaccine; antibody.
XX OS Synthetic.
XX
ID ADK00569 standard; peptide; 45 AA.
XX AC ADK00569;
XX PN WO2004014956-A1.
XX DT 19-FEB-2004.
XX DB Immunogenic lipopeptide of the invention #105.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2003; 2003WO-AU001018.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2002; 2002US-0402838P.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2003; 2003WO-AU001018.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2002; 2002US-0402838P.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

RESULT 6

KW Antinfertility; Vaccine; antibody.
XX OS Synthetic.
XX
ID ADK00569 standard; peptide; 46 AA.
XX AC ADK00569;
XX PN WO2004014956-A1.
XX DT 06-MAY-2004 (first entry)
XX DE Immunogenic lipopeptide of the invention #105.
XX KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
XX Antinfertility; vaccine; antibody.
XX SYnthetic.
XX
PI Jackson D, Zeng W;
XX PN WPI; 2004-238735/22.
XX DR 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.
XX PR 12-AUG-2003; 2003WO-AU001018.
XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

RESULT 5

KW Antinfertility; Vaccine; antibody.
XX OS Synthetic.
XX
ID ADK00571 standard; peptide; 45 AA.
XX AC ADK00571;
XX PN WO2004014956-A1.
XX DT 19-FEB-2004.
XX DB Immunogenic lipopeptide of the invention #107.
XX KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;

X (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.

X Jackson D, Zeng W;

X WPI: 2004-238735/22.

X Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.

X S Claim 39; SEQ ID NO 105; 194pp; English.

X The present invention relates to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequence of T helper cell epitope and B cell epitope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through &ggr; amino group or terminal side chain group of lysine or lysine analog. The peptides are useful in eliciting the production of antibody against an antigenic B cell epitope in a subject, and are useful for antibody production, synthetic vaccine production, diagnostic method employing antibodies and antibody ligands and immunotherapy for veterinary and human medicine. The method efficiently elicits the production of antibody against antigenic B cell epitope. The present sequence represents a novel immunogenic lipopeptide comprising T helper and B cell epitopes.

Q Sequence 46 AA;

```

Query Match      100.0%;   Score 64; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 14; Conservative 0; Mismatches 0; Indels 0;
Y               1 ASREAKKOVEKALE 14
Y               26 ASREAKKOVEKALE 39
b

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RESULT 7

DK00572	DK00572 standard; peptide; 46 AA.
X	ADK00572;
X	ADK00572;
X	06-MAY-2004 (first entry)
X	Immunogenic lipopeptide of the invention #108.
X	T helper cell epitope; B cell epitope; Antibacterial; Antiucler;
X	Antiinfertility; Vaccine; antibody.
X	Synthetic.

N N WO2004014956-A1.
X X 19-FEB-2004.
D D 12-AUG-2003; 2003WO-AU001018.
X X 12-AUG-2002; 2002US-0402838P.
F F (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES
X X

Jackson D, Zeng W;
WPI; 2004-238735/22.
Novel lipopeptide comprising polypeptide having amino acid sequence of T helper cell epitope and B cell epitope, conjugated to lipid moieties, useful for eliciting immune response against group A Streptococcus antigen.

XX Claim 39; SEQ ID NO 108; 194pp; English.
 PS
 XX The present invention relates to a lipopeptide comprising polypeptide
 CC conjugated to lipid moieties, where polypeptide contains amino acid
 CC sequence of T helper cell epitope and B cell epitope, where amino acid
 CC sequences are different, and internal lysine residues or internal lysine
 CC analog residues for covalent attachment of each of lipid moieties through
 CC è amino group or terminal side chain group of lysine or lysine
 CC analog. The peptides are useful in eliciting the production of antibody
 CC against an antigenic B cell epitope in a subject, and are useful for
 CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.
 XX Sequence 46 AA;
 SQ Query Match 100.0%; Score 64; DB 8; Length 46;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASPREAKKOVYEKALE 14

RESULT 8
ADK00570
ID ADK00570 standard; peptide; 47 AA.

AC	ADK00570;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Immunogenic lipopeptide of the invention #106.
XX	
KW	T helper cell epitope; B cell epitope; Antibacterial; Anticancer;
KW	Antinfertility; Vaccine; antibody.
XX	
OS	Synthetic.
XX	
PN	WO2004014956-A1.
XX	
PD	19-FEB-2004.
XX	
PF	12-AUG-2003; 2003WO-AU001018.
XX	
PR	12-AUG-2002; 2002US-0402833P.
XX	
PA	(CONN-) COUNCIL QUEENSLAND INST MEDICAL RES.

XX XX Jackson D, Zeng W;
XX DR WPI; 2004-238735/22.
XX PT Novel lipopeptide comprising polypeptide having amino acid sequence of T
PR helper cell epitope and B cell epitope, conjugated to lipid moieties,
PR useful for eliciting immune response against group A Streptococcus
PR antigen.
XX PS Claim 39; SEQ ID NO 106; 194PP; English.
XX CC The present invention relates to a lipopeptide comprising polypeptide
CC conjugated to lipid moieties, where polypeptide contains amino acid
CC sequence of T helper cell epitope and B cell epitope, where amino acid
CC sequences are different, and internal lysine residues or internal lysine
CC analog residues for covalent attachment of each of lipid moieties through
CC & terminal side chain group of lysine or lysine
CC analog. The peptides are useful in eliciting the production of antibodies
CC against an antigenic B cell epitope in a subject, and are useful for

CC antibody production, synthetic vaccine production, diagnostic method
 CC employing antibodies and antibody ligands and immunotherapy for
 CC veterinary and human medicine. The method efficiently elicits the
 CC production of antibody against antigenic B cell epitope. The present
 CC sequence represents a novel immunogenic lipopeptide comprising T helper
 CC and B cell epitopes.

XX Sequence 47 AA;

Query Match Score 64; DB 8; Length 47;
 Best Local Similarity 100.0%; Pred. No. 0.0048;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 Db 27 ASREAKKQVEKALE 40
 Sequence 234 AA;

RESULT 9

ARL0221
 ID ARL0221 standard; protein; 234 AA.
 XX

AC AAR0221;
 XX

DT 25-MAR-2003 (revised)
 DT 26-MAR-1991 (first entry)

XX

DB Streptococcal M6' protein.

XX

KW Streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus;
 poxvirus; vaccine; streptococcal pharyngitis.

XX

OS Streptococcus sp.

XX

PN WO9015872-A.

XX

PD 27-DEC-1990.

XX

PP 21-JUN-1989;

XX

PR 21-JUN-1989;

XX

PR 19-JUN-1990;

XX

PA (UYR) UNIV ROCKEFELLER.

PA (UTOR) UNIV OREGON STATE.

XX

PI Fischetti VA, Kruby DE;

XX

WPI: 1991-022236/03.

DR N-PSDB; AAQ10244.

XX

PT New recombinant streptococcal M protein DNA and viral vector - for
 production of poxviridae vaccines in treatment of vaccinia, fowlpox etc.

XX

PS Disclosure; Fig 5; 41pp; English.

XX This M'6 protein corresponds to the conserved exposed polypeptide region
 CC of the streptococcal M protein. It is encoded by a genetically
 CC engineered gene introduced into the genome of a vaccinia or fowlpox
 CC virus. The resultant DNA complex is useful as a vaccine for
 CC immunoprotection against streptococcal infections. The M'6 polypeptide is
 CC the part of protein M responsible for virulence. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 234 AA;

Query Match Score 64; DB 2; Length 234;

Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 85 ASREAKKQVEKALE 98

RESULT 10

AAB03118

ID AAB03118 standard; protein; 236 AA.

XX

AC AAB03118;

XX

DT 10-OCT-2000 (first entry)

XX

DB C-terminus of Streptococcus pyogenes M protein M5.

XX

Multivalent hybrid M protein; M5; group A streptococcus; serotype;

KW immunogenic; sero-specific antibody; streptococcal infection;

KW cross reactivity; vaccine; acute rheumatic fever; ARF;

KW rheumatic heart disease; streptococcal pharyngitis; strep throat;

XX

Streptococcus pyogenes.

XX

US6063386-A.

XX

PD 16-MAY-2000.

XX

PF 15-SEP-1997;

XX

PR 16-SEP-1992;

XX

(UTSE-) UNIV TENNESSEE RES CORP.

XX

PI Lederer JW, Dale JB;

XX

DR WPI; 2000-364475/31.

XX

New immunogenic recombinant hybrid M protein comprising amino-terminal

peptide fragments of streptococcal M protein useful as vaccine against

rheumatic fever and infections leading to rheumatic fever.

XX

Disclosure; Col 45-46; 62pp; English.

XX

The invention relates to multivalent immunogenic hybrid group A

streptococcal M proteins comprising N-terminal peptide fragments of M

proteins that elicit opsonic antibodies against multiple serotypes of

group A streptococci (e.g., Streptococci pyogenes). The antibodies

generated using the hybrid proteins are against one or more M protein

serotypes, where at least one of the serotypes is M1, M3, M18 or M19. The

invention also encompasses a recombinant DNA molecule comprising a

nucleotide sequence that encodes a multivalent hybrid M protein; and a

method for immunising a mammal against streptococcal infections,

comprising administering an immunogenic multivalent hybrid M protein to

the mammal. The multivalent hybrid M proteins are useful for eliciting

opsonic or protective antibodies to the M proteins of different serotypes

of group A streptococci, and may therefore be used as vaccines to protect

against and control infection by type A streptococci. Type A streptococci

are not only responsible for streptococcal pharyngitis (strep throat),

forms of pneumonia and a condition resembling toxic shock, but are also

involved in the development of acute rheumatic fever (ARF) and rheumatic

heart disease. In a patient with ARF, antibodies formed during a group A

streptococcal infection are also cross-reactive with heart tissue, which

indicates that the streptococci and host tissue contain similar antigenic

motifs. The new multivalent vaccines are capable of raising sero-specific

antibodies against various serotypes of group A streptococci which are

not cross-reactive with human heart tissue. The present sequence

represents the C-terminal half of the Streptococcus pyogenes M5 protein,

AAW03117

Sequence 236 AA;

XX

Query Match Score 64; DB 3; Length 236;

Best Local Similarity 100.0%; Pred. No. 0.026;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1 ASREAKKQVEKALE 14	AC	AAR20128;
Db	87 ASREAKKQVEKALE 100	XX	XX 27-AUG-2003 (revised)
		DT	DT 15-APR-1992 (first entry)
RESULT 1.1			
AAR50228	AAR50228 standard; protein; 254 AA.	XX	Sequence encoded by truncated M1 gene.
ID		XX	KW Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.
XX		XX	
AC	Streptococcus sp.	OS	
XX		XX	
XX	Location/Qualifiers		
DE	1 .28		
DR	/label= P16M1		
DT	Sequence of a fragment of Group A streptococcal surface protein M5 and a	FT	
DT	carrier of the COOH-terminal portion of M5.	Region	
XX	DE	FT	
XX	B subunit; labile toxin; M protein; fusion protein; antigen;	FT	
KW	Group A streptococci; rheumatic fever; pharyngitis.	FT	
XX	XX	Region	
OS	Streptococcus sp.	FT	
PN	W09406165-A1.	FT	
XX		Region	
XX	PD 31-MAR-1994.	XX	
XX	PN W09119740-A.	PN	
PF	XX	XX	
XX	15-SEP-1993 ; 93WO-US008704.	PD	
PR	XX	XX	
XX	16-SEP-1992 ; 92US -00345860.	PP	
PA	XX	XX	
(UYTE-) UNIV TENNESSEE RES CORP.	PA	PR	
XX	XX	XX	
PI	Dale JB;	PA (HIGH-) HIGHTECH RECEPTOR A.	
XX	XX	PA	
DR	WPI ; 1994-1118162/14.	PI	
N-PSDB; AAQ45160.	XX	Schmidt KH, Akesson P, Cooney J, Bjorck L;	
PT	XX	XX	
New recombinant hybrid streptococcal M protein antigen(s) - which elicit	XX	WPI : 1992-024366/03.	
PT opionic antibodies without eliciting cross-reactive antibodies to	XX	DR N-PSDB; AAQ20292.	
mammalian heart tissue.	XX	PT New IgG binding proteins H' lacking an albumin binding sequence - useful	
PS Disclosure; Fig 4 ; 45pp; English.	XX	PT in purificn. of excess IgG from blood and to diagnose autoimmune	
XX	XX	PT diseases.	
CC The surface M protein of Group A streptococci is the major virulence	XX	XX Disclosure; Fig 8 ; 37pp; English.	
CC factor and protective antigen of these organisms. However, there are a	XX	CC The inventors claim a protein prod. by a strain of Gp.A Streptococci.	
CC tremendous number of M protein serotypes. The invention provides	CC	CC The protein has the AA sequence of protein H but lacks at least some part of	
CC recombinant M protein comprising a gene encoding a carrier	CC	CC the C and D regions (responsible for binding albumin), esp. it lacks the	
CC protein and an NH2 or COOH terminal M protein fragment carrying one or	CC	CC whole of these regions and extends for AA1 to AA158.	
CC more epitopes. The carrier may be the B subunit of E. coli labile toxin	CC	CC Compared with a natural protein H, it is more specific and may be used as part of a kit	
CC (LT-B) or the C-repeat portion of a streptococcal M protein. For example,	CC	CC for the binding, separation and identification of human IgG. The same	
CC AAC45160/R50228 comprises an antigen which is an M5 hapten fragment of 16	CC	CC sequences appear in W09119741. (Updated on 27-AUG-2003 to correct OS	
CC amino acids joined by a BamHI restriction site to a carrier which is the COOH-	CC	CC field.)	
CC terminal half of M5. The carrier includes 2.5 C repeats, which each	XX	XX Sequence 281 AA;	
CC commence with the tetrapeptide NKIS. A linker could be inserted at the	CC	Query Match Score 100.0%; DB 2; Length 281;	
CC BamHI site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-	CC	Best Local Similarity 100.0%; Pred. No. 0.032;	
CC AUG-2003 to correct OS field.)	XX	Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Sequence 254 AA;	Qy 1 ASREAKKQVEKALE 14	Db 132 ASREAKKQVEKALE 145	
	Best Local Similarity 100.0%; Pred. No. 0.028;	RESULT 1.3	
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Db AAR50229	ID AAR50229	
Db 105 ASREAKKQVEKALE 118	AC	AC	
	Db AAR50229;	XX	
	DT 27-AUG-2003 (revised)	AC	
RESULT 1.2			
AAR20128	AAR20128 standard; protein; 281 AA.	XX	
ID		AC	
XX		XX	

DT 25-MAR-2003 (revised)
 DT 09-OCT-1994 (first entry)
 XX Sequence of fragments of Group A streptococcal surface protein M5 and a carrier of the COOH-terminal portion of M5.
 XX B subunit; labile toxin; M protein; fusion protein; antigen;
 KW Group A streptococci; rheumatic fever; pharyngitis.
 XX Streptococcus sp.
 OS WO9106465-A1.
 PN 16-SEP-1992; 92US-00945860.
 XX PA (UTTE-) UNIV TENNESSEE RES CORP.
 XX PD 31-MAR-1994.
 PF 15-SEP-1993; 93WO-US008704.
 XX DR WPI; 1994-118162/14.
 DR N-PSDB; AAQ45161.
 XX PT New recombinant hybrid streptococcal M protein antigen(s) - which elicit opsonic antibodies without eliciting cross-reactive antibodies to PT mammalian heart tissue.
 XX Disclosure: Fig 5; 45PP; English.
 CC The surface M protein of Group A streptococci is the major virulence factor and protective antigen of these organisms. However, there are a tremendous number of M protein serotypes. The invention provides recombinant M protein antigens comprising a gene encoding a carrier protein and an NH₂ or COOH terminal M protein fragment carrying one or more epitopes. The carrier may be the B subunit of E. coli labile toxin (LT-B) or the C-repeat portion of a streptococcal M protein. For example, AAQ45161-R5029 comprises three segments of M5 designated A, B and C. The C segment is joined by a BamHI restriction site to a carrier which is the COOH-terminal half of M5. The carrier includes 2.5 c-repeats, which each commence with the tetrapeptide NKIS. A linker could be inserted at the BamHI site. (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to correct OS field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX SQ Sequence 284 AA;
 Query Match 100.0%; Score 64; DB 2; Length 284;
 Best Local Similarity 100.0%; Pred. No. 0.032;
 Matches 14; Conservative 0; N mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 Db 135 ASREAKKQVEKALE 148

RESULT 14
 AAR50996 AAR50996 standard; protein; 305 AA.
 ID AAR50996;
 AC AAR50996;
 DT 25-MAR-2003 (revised)
 DT 02-NOV-1994 (first entry)
 XX Recombinant M24-M5-M6-M19 C-term variant.

XX Primer; PCR; amplify; polymerase chain reaction; construct; hybrid;
 KW M protein; M24; M5; M6; M19; subunit; tetravalent protein; emm gene;
 KW tandem; PKK223.3; protective epitope; tissue-cross-reactive epitope;
 KW restriction enzyme site; multivalent M protein; immunisation; group A;
 KW streptococci; rheumatic fever; rheumatic heart disease; humoral;

KW antibody; heart tissue; antigen; serotype; mucosal.
 XX Synthetic.
 OS Location/Qualifiers
 XX 1.; 1.18
 FH Key Peptide /label= M24
 FT Peptide 19.; .35
 FT Peptide /label= M5
 FT Peptide 36.; .52
 FT Peptide /label= M6
 FT Peptide 51.; .69
 FT Peptide /label= M19
 FT Peptide 70.; .305
 FT Peptide /label= M5 C-terminal fragment
 XX WO9106421-A1.
 PN 16-SEP-1992; 92US-00945954.
 XX (UTTE-) UNIV TENNESSEE RES CORP.
 PD 31-MAR-1994.
 XX PI 15-SEP-1993; 93WO-US008703.
 PF 15-SEP-1993; 93WO-US008703.
 XX PR 16-SEP-1992; 92US-00945954.
 XX DR WPI; 1994-118122/14.
 DR N-PSDB; AAQ45218.
 XX PT New immunogenic hybrid proteins derives from streptococcal M proteins - PT induces opsonic antibodies, for protective immunisation against multiple group A streptococci serotypes.
 PS Disclosure; Fig B; 67pp; English.
 XX CC The sequences given in AAR50992-1-1001 represent hybrid M proteins which contain the M24-M5-M6 and/or M19 subunits. These multivalent proteins were constructed using fragments of the 5' regions of emm genes that were amplified by PCR, ligated in tandem and expressed in pKK223.3. The amplified regions pref. encode protective and not tissue-cross-reactive epitopes, which can then be linked into one protein molecule. The recombinant hybrid protein may contain 113 N-terminal amino acids of M24, 58 amino acids of M5, 35 from M6 and 35 from M19. Each section is linked by 2 amino acids specified by the respective restriction enzyme sites CC that were synthesised into the primers used to specify the PCR product.
 CC Multivalent M proteins such as this may be used for protective CC immunisation against group A streptococci, which esp. cause rheumatic fever and rheumatic heart disease. Humoral antibodies raised against CC these proteins do not react with heart tissue antigens but are effective CC against many different serotypes. The multivalent proteins may also CC include sequences which induce mucosal antibodies and do not require CC coupling to an immunogenic carrier. (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 305 AA;
 Query Match 100.0%; Score 64; DB 2; Length 305;
 Best Local Similarity 100.0%; Pred. No. 0.034;
 Matches 14; Conservative 0; N mismatches 0; Indels 0; Gaps 0;
 Qy 1 ASREAKKQVEKALE 14
 Db 156 ASREAKKQVEKALE 169

RESULT 15
 AAB03117 AAB03117 standard; protein; 305 AA.
 ID AAB03117;
 XX AC AAB03117;
 AC AAB03117;

Job time : 79.7907 sec

DR 10-OCT-2000 (first entry)

XX S. pyogenes hybrid M protein (M24-M5-M6-M19), SEQ ID NO:10.

DE Multivalent hybrid M protein; group A streptococcus; serotype;

XX immunogenic; sero-specific antibody; streptococcal infection;

XX cross reactivity; vaccine; acute rheumatic fever; ARF;

XX rheumatic heart disease; streptococcal pharyngitis; strep throat;

XX pneumonia.

XX Streptococcus pyogenes .

OS Synthetic.

XX PN US6063186-A.

XX PD 16-MAY-2000.

XX PF 15-SEP-1997; 97US-00937271.

XX PR 16-SEP-1992; 92US-00945954.

XX PA (UYTE-) UNIV TENNESSEE RES CORP.

PI Lederer JW, Dale JB;

XX DR 2000-364475/31.

XX DR N-PSDB; ARA57897.

PR New immunogenic recombinant hybrid M protein comprising amino-terminal peptide fragments of streptococcal M protein useful as vaccine against

PR rheumatic fever and infections leading to rheumatic fever.

XX Disclosure; Fig 8A-B; 62pp; English.

PS

XX The invention relates to multivalent immunogenic hybrid group A streptococcal M proteins comprising N-terminal peptide fragments of M proteins that elicit opsonic antibodies against multiple serotypes of group A streptococci (e.g. Streptococcus pyogenes). The antibodies generated using the hybrid proteins are against one or more M protein serotypes, where at least one of the serotypes is M1, M3, M18 or M19. The invention also encompasses a recombinant DNA molecule comprising a nucleotide sequence that encodes multivalent hybrid M protein; and a method for immunising a mammal against streptococcal infections, comprising administering an immunogenic multivalent hybrid M protein to the mammal. The multivalent hybrid M proteins are useful for eliciting opsonic or protective antibodies to the M proteins of different serotypes of group A streptococci, and may therefore be used as vaccines to protect against and control infection by type A streptococci. Type A streptococci are not only responsible for streptococcal pharyngitis (strep throat), forms of pneumonia and a condition resembling toxic shock, but are also involved in the development of acute rheumatic fever (ARF) and rheumatic heart disease. In a patient with ARF, antibodies formed during a group A streptococcal infection are also cross-reactive with heart tissue, which indicates that the streptococci and host tissue contain similar antigenic motifs. The new multivalent vaccines are capable of raising sero-specific antibodies against various serotypes of group A streptococci which are not cross-reactive with human heart tissue. Sequences AAB0311-B03117, AAB0319-B03121 and AAB03122-B03124 represent multivalent hybrid Streptococcus pyogenes M proteins generated in the disclosure of the invention

XX Sequence 305 AA;

Query Match	100.0%	Score	64;	DB	3;	Length	305;			
Best Local Similarity	100.0%	Pred.	No.	0.034;	Mismatches	0;	Indels	0;	Gaps	0;
Matches	14;	Conservative	0;							

Qy 1 ASREAKKQVEKALE 14

Db 156 ASREAKKQVEKALE 169

Search completed: August 4, 2005, 08:59:23

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OM protein - protein search, using SW model

Run on: August 4, 2005, 08:27:17 ; Search time 19.5349 Seconds

(without alignments)
53.498 Million cell updates/secTitle: US-10-706-275-1
Perfect score: 64
Sequence: 1 ASREAKQVEKALE 14Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cgcn2_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cgcn2_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cgcn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cgcn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cgcn2_6/ptodata/1/iaa/PCUS_COMB.pep:
 6: /cgcn2_6/ptodata/1/iaa/backfile1.pep:
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	64	100.0	20	3	US-08-817-811-1	Sequence 1, Appli
2	64	100.0	236	3	US-08-937-271-11	Sequence 11, Appli
3	64	100.0	254	4	US-08-914-479A-4	Sequence 4, Appli
4	64	100.0	284	4	US-08-914-479A-6	Sequence 6, Appli
5	64	100.0	305	3	US-08-937-271-10	Sequence 10, Appli
6	64	100.0	440	4	US-08-302-756E-35	Sequence 35, Appli
7	64	100.0	443	2	US-08-795-475-6	Sequence 6, Appli
8	64	100.0	443	4	US-08-325-278B-6	Sequence 34, Appli
9	56	87.5	12	3	US-08-817-811-34	Sequence 11, Appli
10	55	85.9	12	3	US-08-817-811-11	Sequence 11, Appli
11	55	85.9	12	3	US-08-817-811-12	Sequence 32, Appli
12	55	85.9	12	3	US-08-817-811-33	Sequence 33, Appli
13	52	81.2	28	3	US-08-817-811-18	Sequence 18, Appli
14	51	79.7	12	3	US-08-817-811-31	Sequence 31, Appli
15	47.5	74.2	28	3	US-08-817-811-17	Sequence 17, Appli
16	46	71.9	12	3	US-08-817-811-10	Sequence 10, Appli
17	46	71.9	12	3	US-08-817-811-12	Sequence 32, Appli
18	46	71.9	20	3	US-08-817-811-38	Sequence 38, Appli
19	44.5	69.5	28	3	US-08-817-811-16	Sequence 16, Appli
20	43	67.2	94	3	US-08-937-271-18	Sequence 18, Appli
21	43	67.2	343	3	US-08-937-271-17	Sequence 17, Appli
22	43	67.2	6	5210183-3	Patent No. 5210183	
23	43	67.2	683	6	5210183-3	Patent No. 5210183
24	42	65.6	65	1	US-08-464-531-83	Sequence 83, Appli
25	42	65.6	65	2	US-08-461-598-83	Sequence 83, Appli
26	42	65.6	65	3	US-08-322-137-83	Sequence 83, Appli
27	42	65.6	380	3	US-08-307-896-1	Sequence 1, Appli

ALIGNMENTS

RESULT 1	US-08-817-811-1	Sequence 1, Application US/08817811
		; Patent No. 6174328
		; GENERAL INFORMATION:
		; APPLICANT: Cooper, Juan A.
		; APPLICANT: Relf, Wendy A.
		; APPLICANT: Good, Michael F.
		; APPLICANT: Saul, Allan J.
		; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
		; NUMBER OF SEQUENCES: 97
		; CORRESPONDENCE ADDRESS:
		; ADDRESSEE: Arnold White & Durkee
		; STREET: P.O. Box 4433
		; CITY: Houston
		; STATE: Texas
		; COUNTRY: USA
		; ZIP: 77210 USA
		; COMPUTER READEABLE FORM:
		; MEDIUM TYPE: Floppy disk
		; COMPUTER: IBM PC compatible
		; OPERATING SYSTEM: PC-DOS/MS-DOS
		; SOFTWARE: PatentIn Release #1.0, Version #1.3.0
		; CURRENT APPLICATION DATA:
		; APPLICATION NUMBER: US/08/817,811
		; FILING DATE: 14-APR-1997
		; CLASSIFICATION: 424
		; PRIOR APPLICATION DATA:
		; APPLICATION NUMBER: WO 96/11944
		; FILING DATE: 25-APR-1996
		; ATTORNEY/AGENT INFORMATION:
		; NAME: Highlander, Steven L.
		; REGISTRATION NUMBER: 37,642
		; REFERENCE/DOCKET NUMBER: FBRC-005
		; TELECOMMUNICATION INFORMATION:
		; TELEPHONE: 512/474-7577
		; TELEFAX: 512/474-7577
		; INFORMATION FOR SEQ ID NO: 1:
		; SEQUENCE CHARACTERISTICS:
		; LENGTH: 20 amino acids
		; TYPE: amino acid
		; STRANDEDNESS:
		; TOPOLOGY: linear
		; US-08-817-811-1
		; Query Match 100.0%; Score 64; DB 3; Length 20;
		; Best Local Similarity 100.0%; Pred. No. 0.0068;
		; Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,271
; FILING DATE: 15-SEP-1997
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Roseman, Stephen J.
; REGISTRATION NUMBER: 43,058
; REFERENCE/DOCKET NUMBER: 481112.4 05C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 305 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-937-271-10

Query Match 100.0%; Score 64; DB 3; Length 305;
Best Local Similarity 100.0%; Pred. No. 0.011; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 156 ASREAKKQVEKALE 16

RESULT 6
US-08-302-756E-35
; Sequence 35, Application US/08302756E
; Patent No. 6737521

GENERAL INFORMATION:
; APPLICANT: FISCHETTI, Vincent A.
; ATTORNEY: POZZI, Gianni
; SCHEINWIND, Olaf
; TITLE OF INVENTION: DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON THE SURFACE OF GRAM POSITIVE BACTERIA
; FILE REFERENCE: 016921-076

CURRENT APPLICATION NUMBER: US/08/302,756B
CURRENT FILING DATE: 1995-03-07
PRIORITY FILING DATE: 1990-05-11
PRIOR APPLICATION NUMBER: US 07/742,199
PRIOR FILING DATE: 1991-08-05
PRIOR APPLICATION NUMBER: US 07/814,823
PRIOR FILING DATE: 1991-12-13
PRIOR APPLICATION NUMBER: US 07/851,082
PRIOR FILING DATE: 1992-03-13
PRIOR APPLICATION NUMBER: PCT/US93/02355
PRIOR FILING DATE: 1993-03-12
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 35
LENGTH: 440
TYPE: PRT
ORGANISM: S. pyogenes

US-08-302-756B-35

Query Match 100.0%; Score 64; DB 4; Length 440;
Best Local Similarity 100.0%; Pred. No. 0.016; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 292 ASREAKKQVEKALE 305

RESULT 7
US-08-795-475-6
; Sequence 6, Application US/08795475
; Patent No. 5965390

GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; ATTORNEY: Svbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SEED and BERRY LLP
; STREET: 6300 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,475
; FILING DATE: 11-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 1000084.402D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 6;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-475-6

Query Match 100.0%; Score 64; DB 2; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.016; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 294 ASREAKKQVEKALE 307

RESULT 8
US-08-325-278B-6
; Sequence 6, Application US/08325278B
; Patent No. 6822075

GENERAL INFORMATION:
; APPLICANT: Björck, Lars
; Sjöbring, Ulf
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Seed IP Law Group
; STREET: 701 Fifth Avenue Suite 6200
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325,278B
; FILING DATE: 26-Oct-1994
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Potter, Jane E. R.
; REGISTRATION NUMBER: 33,332

REFERENCE/DOCKET NUMBER: 100084.402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 6;
 SEQUENCE CHARACTERISTICS:
 LENGTH: 443 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 6;
 US-08-325-278B-6

Query Match 100.0% Score 64; DB 4; Length 443;
 Best Local Similarity 100.0%; Prod. No. 0.016; Mismatches 0; Indels 0; Gaps 0;
 Matches 14; Conservative 0; Number of Sequences: 97

Qy 1 ASREAKKQVEKALE 14
 Db 294 ASREAKKQVEKALE 307

RESULT 9
 US-08-817-811-34 Application US/08817811
 ; Sequence 34, Application US/08817811
 ; Patent No. 617528
 GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: PBRC:005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/471-7577
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-817-811-11

Query Match 95.9% Score 55; DB 3; Length 12;
 Best Local Similarity 100.0%; Prod. No. 0.0074; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of Sequences: 97

Qy 1 ASREAKKQVEKA 12
 Db 1 ASREAKKQVEKA 12

RESULT 11
 US-08-817-811-32 Application US/08817811
 ; Sequence 32, Application US/08817811
 ; Patent No. 617528
 GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; APPLICANT: Relf, Wendy A.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Saul, Allan J.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee

Query Match 87.5% Score 56; DB 3; Length 12;
 Best Local Similarity 100.0%; Prod. No. 0.0074; Mismatches 0; Indels 0; Gaps 0;
 Matches 12; Conservative 0; Number of Sequences: 97

Qy 3 REAKKQVEKALE 14

STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: FBRC:005
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 32:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 STRANDEDNESS: Linear
 US-08-817-811-32

Query Match 85.9%; Score 55; DB 3; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.011;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ASREAKQVEKA 13
 Db 1 ASREAKQVEKA 12

RESULT 13
 US-08-817-811-18
 Sequence 18, Application US/08817811
 Patent No. 6174548
 GENERAL INFORMATION:
 APPLICANT: Cooper, Juan A.
 APPLICANT: Reif, Wendy A.
 APPLICANT: Good, Michael F.
 APPLICANT: Saul, Allan J.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 NUMBER OF INVENTIONS: COMPRISING SAME
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 COUNTRY: USA
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: FBRC:005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 18:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS: Linear
 TOPOLOGY: Linear
 US-08-817-811-18

Query Match 81.2%; Score 52; DB 3; Length 28;
 Best Local Similarity 78.6%; Pred. No. 0.075%;
 Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
 | :|||:|||:|||:|||:
 Db 10 ASREAKKQVEKVK 23

RESULT 14
 US-08-8117-811-31
 ; Sequence 31, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; Ref., Wendy A.
 ; APPLICANT: Good, Michael P.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Arnold, White & Durkee
 ; STREET: P. O. Box 4433
 ; CITY: Houston
 ; STATE: Texas
 ; COUNTRY: USA
 ; ZIP: 77210

COMPUTER READABLE FORM:
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/8117,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: FBRC:005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 17:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-8117-811-17

Query Match 74.2%; Score 47.5; DB 3; Length 28;
 Best Local Similarity 76.5%; Pred. No. 0.38;
 Matches 13; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

Qy 1 ASREAKKQVE--KALE 14
 Db 11 ASREAKKQVEDKVQLKE 27

Search completed: August 4, 2005, 08:38:31
 Job time : 20.5349 secs

Qy 1 ASREAKKQVEK 11
 Db 2 ASREAKKQVEK 12

RESULT 15
 US-08-8117-811-17
 ; Sequence 17, Application US/08817811
 ; Patent No. 6174528
 ; GENERAL INFORMATION:
 ; APPLICANT: Cooper, Juan A.
 ; Ref., Wendy A.
 ; APPLICANT: Good, Michael P.
 ; APPLICANT: Saul, Allan J.
 ; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 ; TITLE OF INVENTION: COMPRISING SAME
 ; NUMBER OF SEQUENCES: 97
 ; CORRESPONDENCE ADDRESS:


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Qy      1 ASREAKKQVEKALE 14          Query Match      100.0%; Score 64; DB 17; Length 20;
Db      1 ASREAKKQVEKALE 14          Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
US-10-044-034-22 Application US/10044034
; Sequence 22, Application US/10044034
; GENERAL INFORMATION:
;   APPLICANT: JACKSON, DAVID C.
;   APPLICANT: O'BRIEN-SIMPSON, NEIL M.
;   APPLICANT: BROWN, LORENA E.
;   APPLICANT: EDE, NICHOLAS J.
;   APPLICANT: GOOD, MICHAEL F.
;   APPLICANT: BRANDT, EVELYN R.
;   TITLE OF INVENTION: POLYMERS INCORPORATING PEPTIDES
;   FILE REFERENCE: FBRC-006
;   CURRENT APPLICATION NUMBER: US/10/044, 034
;   CURRENT FILING DATE: 2002-01-11
;   PRIOR APPLICATION NUMBER: P05071
;   PRIOR FILING DATE: 1997-02-11
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO: 22
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;   OTHER INFORMATION: Peptides
US-10-044-034-22

Qy      1 ASREAKKQVEKALE 14          Query Match      100.0%; Score 64; DB 13; Length 20;
Db      1 ASREAKKQVEKALE 14          Best Local Similarity 100.0%; Pred. No. 0.0035; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
US-10-706-275-5 Application US/10706275
; Sequence 5, Application US/10706275
; GENERAL INFORMATION:
;   APPLICANT: ID Biomedical Corporation of Quebec
;   APPLICANT: The Council of the Queensland Institute of Medical Research
;   APPLICANT: Lowell, George H.
;   APPLICANT: Burt, David S.
;   APPLICANT: White, Gregory L.
;   APPLICANT: Good, Michael F.
;   APPLICANT: Batzloff, Michael R.
;   APPLICANT: Leandersson, Tomas B.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: 1-989-000710US
;   CURRENT FILING DATE: 2003-11-13
;   PRIOR APPLICATION NUMBER: US 60/426, 409
;   PRIOR FILING DATE: 2002-11-15
;   NUMBER OF SEQ ID NOS: 15
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO: 5
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen
US-10-706-275-5

Qy      1 ASREAKKQVEKALE 14          Query Match      100.0%; Score 64; DB 17; Length 29;
Db      7 ASREAKKQVEKALE 20          Best Local Similarity 100.0%; Pred. No. 0.0051; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
US-10-706-275-2
; Sequence 2, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
;   APPLICANT: ID Biomedical Corporation of Quebec
;   APPLICANT: The Council of the Queensland Institute of Medical Research
;   APPLICANT: Lowell, George H.
;   APPLICANT: Burt, David S.
;   APPLICANT: White, Gregory L.
;   APPLICANT: Good, Michael F.
;   APPLICANT: Batzloff, Michael R.
;   APPLICANT: Leandersson, Tomas B.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: 021989-000710US
;   CURRENT APPLICATION NUMBER: US/10/044, 034
;   CURRENT FILING DATE: 2003-11-13
;   PRIOR APPLICATION NUMBER: US 60/426, 409
;   PRIOR FILING DATE: 1997-02-11
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO: 2
;   LENGTH: 29
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antigenic peptide derivative of S. pyogenes with flanking sequen
US-10-706-275-2

Qy      1 ASREAKKQVEKALE 14          Query Match      100.0%; Score 64; DB 17; Length 29;
Db      9 ASREAKKQVEKALE 22          Best Local Similarity 100.0%; Pred. No. 0.0051; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
US-10-706-275-15
; Sequence 15, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
;   APPLICANT: ID Biomedical Corporation of Quebec
;   APPLICANT: The Council of the Queensland Institute of Medical Research
;   APPLICANT: Lowell, George H.
;   APPLICANT: Burt, David S.
;   APPLICANT: White, Gregory L.
;   APPLICANT: Good, Michael F.
;   APPLICANT: Batzloff, Michael R.
;   APPLICANT: Leandersson, Tomas B.
;   TITLE OF INVENTION: Vaccine
;   FILE REFERENCE: 021989-000710US
;   CURRENT APPLICATION NUMBER: US/10/044, 034
;   CURRENT FILING DATE: 2003-11-13
;   PRIOR APPLICATION NUMBER: US 60/426, 409
;   PRIOR FILING DATE: 1997-02-11
;   NUMBER OF SEQ ID NOS: 28
;   SOFTWARE: PatentIn version 3.1
;   SEQ ID NO: 5
;   LENGTH: 20
;   TYPE: PRT
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: antigenic peptide sequence p145
;   NUMBER OF SEQ ID NOS: 15
US-10-706-275-5

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SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 15
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-15

Query Match Score 64; DB 17; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.0051;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 9 ASREAKKQVEKALE 22

RESULT 6
US-10-141-627-4
; Sequence 4, Application US/10141627
; GENERAL INFORMATION:
; Publication No. US20020176863A1
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE REFERENCE: 481112..40C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 4
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of M5 and a carrier of the
; OTHER INFORMATION: COOH-terminal portion of M5
US-10-141-627-4

Query Match Score 64; DB 13; Length 254;
Best Local Similarity 100.0%; Pred. No. 0.049;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 105 ASREAKKQVEKALE 118

RESULT 7
US-10-141-627-6
; Sequence 6, Application US/10141627
; GENERAL INFORMATION:
; Publication No. US20020176863A1
; APPLICANT: Dale, James B.
; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
; FILE REFERENCE: 481112..40C3
; CURRENT APPLICATION NUMBER: US/10/141,627
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 6
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
; OTHER INFORMATION: of the COOH-terminal portion of M5
US-10-141-627-6

Query Match Score 64; DB 13; Length 284;
Best Local Similarity 100.0%; Pred. No. 0.055;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 135 ASREAKKQVEKALE 148

RESULT 8
US-08-325-278-6
; Sequence 6, Application US/08325278
; Publication No. US2003027283A1
; GENERAL INFORMATION:
; APPLICANT: Bivrck, Lars
; APPLICANT: Sjibring, Olle
; TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSE: SEED and BERRY LLP
; STREET: 6360 Columbia Center, 701 Fifth Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZPP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/325-278
; FILING DATE: 26-OCT-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: McMasters, David D.
; REGISTRATION NUMBER: 33,963
; REFERENCE/DOCKET NUMBER: 450023-401
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-5031
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 443 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-325-278-6

Query Match Score 64; DB 8; Length 443;
Best Local Similarity 100.0%; Pred. No. 0.087;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 294 ASREAKKQVEKALE 307

RESULT 9
US-10-474-792-672
; Sequence 672, Application US/10474792
; Publication No. US2004023072A1
; GENERAL INFORMATION:
; FILE REFERENCE: AM 100399
; CURRENT APPLICATION NUMBER: US/10/474,792
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 672
; LENGTH: 553

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; TYPE: PRT ; ORGANISM: Streptococcus pyogenes
US-10-474-792-672
Query Match 100.0%; Score 64; DB 16; Length 553;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 404 ASREAKKQVEKALE 417

RESULT 10
US-10-732-923-3295
; Sequence 3295, Application US/10732923
; Publication No. US20050108791A1
; GENERAL INFORMATION:
; APPLICANT: Edgerton, Michael D
; TITLE OF INVENTION: TRANSGENIC PLANTS WITH IMPROVED PHENOTYPES
; FILE REFERENCE: 38-15(52/96)C
; CURRENT APPLICATION NUMBER: US/10/732,923
; CURRENT FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: 10/310,154
; PRIOR FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 24149
; SEQ ID NO: 3295
; LENGTH: 558
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-732-923-3295

Query Match 100.0%; Score 64; DB 17; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 409 ASREAKKQVEKALE 422

RESULT 11
US-10-706-275-12
; Sequence 12, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-0007100US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 12
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-13

Query Match 100.0%; Score 64; DB 17; Length 558;
Best Local Similarity 100.0%; Pred. No. 0.11; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14
Db 409 ASREAKKQVEKALE 422

RESULT 12
US-10-706-275-13
; Sequence 13, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-0007100US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 14
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-12

Query Match 89.1%; Score 57; DB 17; Length 28;

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; TYPE: PRT          ; PRIOR FILING DATE: 2002-11-15
; ORGANISM: Artificial Sequence ; PRIOR APPLICATION NUMBER: AU 2002302132
; FEATURE:          ; PRIOR FILING DATE: 2002-11-15
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
; US-10-706-275-14 ; NUMBER OF SEQ ID NOS: 15
;                      ; SOFTWARE: PatentIn version 3.1
;                      ; SEQ ID NO: 10
;                      ; LENGTH: 28
;                      ; TYPE: PRT
;                      ; ORGANISM: Artificial Sequence
;                      ; FEATURE:
;                      ; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
; US-10-706-275-10 ; Score 56; DB 17; Length 28;
; Query Match       ; Best Local Similarity 100.0%; Pred. No. 0.087;
; Matches 12;      ; Mismatches 0; Indels 0; Gaps 0;
; Db                ; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
;                      ; Score 47.5%; DB 17; Length 28;
;                      ; Best Local Similarity 76.5%; Pred. No. 1.8%;
;                      ; Matches 13; Conservative 0; Mismatches 1; Indels 3; Gaps 1;
; Qy                ; 1 ASREAKKQVE--TAKLE 14
;                      ; | | | | | | | | | |
;                      ; | | | | | | | | | |
; Db                ; 11 ASREAKKQVEKVKV 27
;                      ; Search completed: August 4, 2005, 08:55:13
;                      ; Job time : 68.3721 secs

RESULT 14
US-10-706-275-11
; Sequence 11, Application US/10706275
; PUBLICATION NO. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael P.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leandersson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
; US-10-706-275-11

Query Match       ; Score 52; DB 17; Length 28;
; Best Local Similarity 78.6%; Pred. No. 0.36%;
; Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Db                ; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
;                      ; Score 81.2%; DB 17; Length 28;
;                      ; Best Local Similarity 81.2%; Pred. No. 0.36%;
;                      ; Matches 11; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
; Qy                ; 1 ASREAKKQVEKALE 14
;                      ; | | | | | | | | | |
;                      ; | | | | | | | | | |
; Db                ; 10 ASREAKKQVEKVK 23

RESULT 15
US-10-706-275-10
; Sequence 10, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION:
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael P.
; APPLICANT: Batzloff, Michael R.
; APPLICANT: Leandersson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:50:19 ; Search time 15.3023 Seconds
 88.028 Million cell updates/sec

Title: US-10-706-275-1
 Perfect score: 64

Sequence: 1 ASREAKQVEKALE 14

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters:

283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	64	100.0	388	A49545	plasminogen-bindin
2	64	100.0	408	S30283	protein M precurso
3	64	100.0	436	S30284	M protein precurso
4	64	100.0	454	S43556	plasminogen-bindin
5	64	100.0	472	S43554	plasminogen-bindin
6	64	100.0	483	A26297	M6 protein - Strep
7	64	100.0	484	S35401	M1 protein precurs
8	64	100.0	484	S46489	M1.1 protein precu
9	64	100.0	484	S34978	M5 protein precurs
10	64	100.0	492	A28616	M protein precurso
11	64	100.0	501	A44643	IgG-binding protei
12	64	100.0	528	S57835	M protein - Strep
13	64	100.0	532	S54871	M24 protein precur
14	64	100.0	539	A28549	M protein precurso
15	64	100.0	564	A60115	FC gamma (IgG) rec
16	64	100.0	587	JC1419	hypothetical protei
17	45	70.3	546	T32382	conserved hypothet
18	44	68.8	149	C81248	hypothetical protei
19	44	68.8	423	T48000	conserved hypothet
20	43	67.2	104	H64327	hypothetical protei
21	43	67.2	168	PH0139	M protein-like mol
22	43	67.2	365	B54128	FC-binding protein
23	43	67.2	384	S49550	M-like protein emm
24	43	67.2	386	S05568	IgA receptor precur
25	43	67.2	386	S54858	M protein precurso
26	43	67.2	389	A43715	M49 protein precur
27	43	67.2	402	S37046	IgA receptor - Str
28	43	67.2	407	S23325	M2 protein precur
29	42	65.6	91	A46685	GTP-binding regula

Qy 1 ASRBAKOVSKALE 14

O;

Gaps 0;

Indels 0;

DB 2;

Length 388;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Mismatches 0;

Prod. No. 0.019;

Best Local Similarity 100.0%;

Score 64;

Query Match 100.0%;

Matches 14;

Conservative 0;

Db 266 ASREAKKQVEKALE 279

RESULT 2

S30283 protein M precursor - Streptococcus pyogenes (serotype M41)

C;Species: Streptococcus pyogenes

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

R;Podbielski, A.

Mol. Gen. Genet. 237, 287-300, 1993

A;Title: Three different types of organization of the vir regulon in group A streptococci

A;Accession: S30283

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-408 <POD>

A;Cross-references: UNIPROT:Q54837; EMBL:X58178

R;Podbielski, A.; Melzer, B.

Submitted to the EMBL Data Library, February 1991

A;Description number: S30283; MUID:93204905; PMID:8455563

A;Reference number: S29680

A;Accession: S29680

A;Molecule type: DNA

A;Residues: 1-230, 'N', 232-371, 'R', 373-408 <POD2>

A;Cross-references: EMBL:X58178; NID:947362; PIDN:CAA41167.1; PID:947363

C;Genetics:

A;Gene: emm

C;Superfamily: M5 protein

C;Keywords: transmembrane protein

F;1-41/Domain: signal sequence #status predicted <SIG>

F;42-408/Product: M protein #status predicted <MAT>

F;383-401/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 64; DB 2; Length 408;

Best Local Similarity 100.0%; Pred. No. 0.02; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 259 ASREAKKQVEKALE 279

RESULT 3

S30284 M protein precursor - Streptococcus pyogenes (serotype M52)

C;Species: Streptococcus pyogenes

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004

R;Podbielski, A.

Mol. Gen. Genet. 237, 287-300, 1993

A;Title: Three different types of organization of the vir regulon in group A streptococci

A;Accession: S30284

A;Status: nucleic acid sequence not shown

A;Molecule type: DNA

A;Residues: 1-436 <POD1>

A;Cross-references: UNIPROT:Q54839; EMBL:X58179

R;Podbielski, A.; Melzer, B.

Submitted to the EMBL Data Library, February 1991

A;Description: PCR mediated cloning and sequencing of group A streptococcal emm41/52 (ev)

A;Reference number: S29680

A;Molecule type: DNA

A;Residues: 1-216, 'N', 218-436 <POD2>

A;Cross-references: EMBL:X58179; NID:947364; PIDN:CAA41168.1; PID:947365

C;Genetics:

A;Gene: emm

C;Superfamily: M5 protein

C;Keywords: transmembrane protein

F;1-41/Domain: signal sequence #status predicted <SIG>

F;42-436/Product: M protein #status predicted <MAT>

F;411-429/Domain: transmembrane #status predicted <TMM>

Query Match 100.0%; Score 64; DB 2; Length 436;

Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 287 ASREAKKQVEKALE 300

RESULT 4

S43556 plasminogen-binding protein MLG36 - Streptococcus sp. (fragment)

C;Species: Streptococcus sp.

C;Accession: S43556; S43556

R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoerbring, U.

Bur. J. Biochem. 222, 267-276, 1994

A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci

A;Reference number: S45598; MUID:94291620; PMID:8020466

A;Accession: S45598

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-454 <BE2>

A;Cross-references: EMBL:232677; NID:9474767; PIDN:CAA83588.1; PID:9474768

C;Superfamily: M5 protein

Query Match 100.0%; Score 64; DB 2; Length 454;

Best Local Similarity 100.0%; Pred. No. 0.022; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 332 ASREAKKQVEKALE 345

RESULT 5

S43554 plasminogen-binding protein MLG72 - Streptococcus sp. (fragment)

C;Species: Streptococcus sp.

A;Variety: group G

C;Accession: S43554; S43554

R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.

Bur. J. Biochem. 222, 267-276, 1994

A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci

A;Reference number: S45598; MUID:94291620; PMID:8020466

A;Accession: S45599

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-472 <BE2>

A;Cross-references: EMBL:232678; NID:9474769; PIDN:CAA83589.1; PID:9474768

C;Superfamily: M5 protein

Query Match 100.0%; Score 64; DB 2; Length 472;

Best Local Similarity 100.0%; Pred. No. 0.023; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKKQVEKALE 14

Db 350 ASREAKKQVEKALE 363

RESULT 6

A26297 M6 protein - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

C;Accession: A26297

R;Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.

J. Biol. Chem. 261, 1677-1686, 1986

A;Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus

A;Reference number: A26297; MUID:86111835; PMID:3511046

A;Accession: A26297
A;Molecule type: DNA
A;Residues: 1-183 <HOL>
C;Cross-references: UNIPROT:P08089; GB:M11338; PIDN:AAA26920.1;
A;Gene: emm6
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein

Query Match 100.0% Score 64; DB 2; Length 483;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKQVEKALE 14
Db 334 ASREAKQVEKALE 347

RESULT 7

M1 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

A;Variety: serotype M1
C;Date: 31-Dec-1993 # sequence revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S35401; S61074; S60784
R;Publistki, A.
Submitted to the EMBL Data Library, September 1991
A;Reference number: S35401
A;Accession: S35401
A;Molecule type: DNA
A;Residues: 1-484 <PDB>
A;Cross-references: UNIPROT:Q10372; EMBL:X62131; PIDN:9311757; PIDN:CBA44062.1; PID:93117
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
Submitted to the EMBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm gene sequences and t
A;Reference number: S61072
A;Accession: S61074
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 16-94 <WHA>
A;Cross-references: EMBL:U11940; PIDN:AAA99556.1; PID:9533558
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:891551
A;Accession: S60784
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 29-89 <WH2>
A;Cross-references: EMBL:U11940
C;Genetics:
A;Gene: emm1
C;Superfamily: M5 protein

Query Match 100.0% Score 64; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKQVEKALE 14
Db 335 ASREAKQVEKALE 348

RESULT 9

M1 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

A;Accession: S34978
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: S34978; S31966
R;Harbaugh, M.P.; Podbleiski, A.; Huegli, S.; Cleary, P.P.
Mol. Microbiol. 8, 981-991, 1993
A;Title: Nucleotide substitutions and small-scale insertion produce size and antigenic
A;Reference number: S34978
A;Accession: S34978
A;Molecule type: DNA
A;Residues: 1-484 <HAR>
A;Cross-references: UNIPROT:Q05464; ENBL:Z21845; NID:949401; PIDN:CAA79893.1; PID:94940
C;Genetics:
A;Gene: emm1.1
C;Superfamily: M5 protein
C;Keywords: membrane protein
F;43-484/Product: M1.1 protein #status predicted <SIG>
Query Match 100.0% Score 64; DB 2; Length 484;
Best Local Similarity 100.0%; Pred. No. 0.024;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREAKQVEKALE 14
Db 335 ASREAKQVEKALE 348

RESULT 10

M5 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

A;Variety: serotype M5
C;Accession: A28616; S66787
R;Miller, L.; Gray, L.; Beachey, E.; Kehoe, M.
J. Biol. Chem. 263, 5668-5673, 1988
A;Title: Antigenic variation among group A streptococcal M proteins. Nucleotide sequenc
A;Reference number: A28616; MUID:8818881; PMID:3281944
A;Accession: A28616
A;Molecule type: DNA
A;Residues: 1-492 <MIL>
A;Cross-references: UNIPROT:P02977; GB:M20374; PIDN:9153812; PID:915381
R;Akesson, P.; Schmidt, K.H.; Cooney, J.; Bjoerck, L.
Biochem. J. 300, 877-886, 1994
A;Title: M1 protein and protein H: IgGc- and albumin-binding streptococcal surface pro
A;Reference number: S46489; MUID:94280417; PMID:8010973

RESULT 8

M1 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes

C;Accession: S46489; S46490
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C;Accession: S46489; S46490
C;Variety: serotype M5
C;Accession: A28616; S66787
R;Akesson, P.; Schmidt, K.H.; Cooney, J.; Bjoerck, L.
Biochem. J. 300, 877-886, 1994
A;Title: M1 protein and protein H: IgGc- and albumin-binding streptococcal surface pro
A;Reference number: S46489; MUID:94280417; PMID:8010973

A;Title: Non-congruent relationships between variation in *emm* gene sequences and the *pop*
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A;Molecule type: DNA
A;Residues: 30-89 <WHA>
C;Genetics:
A;Gene: Smr5
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein
P;1.42/Domain: signal sequence #status predicted <SIG>
P;43-49/Product: M5 protein #status predicted <MAT>,
Query Match 100.0%; Score 64; DB 2; Length 492;
Best Local Similarity 100.0%; Pred. No. 0.024; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
Db 343 ASREAKKQVEKALE 356

RESULT 11

A44643 M protein precursor - *Streptococcus pyogenes* (serotype M57) (fragment)
C;Species: *Streptococcus pyogenes*
A;Variety: serotype M57
C;Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 10-Dec-1999
C;Accession: A44643; S60833
R;Manjula, K.M.; Khandare, T.; Relf, W.A.; Srivakash, K.S.
J;Protein Chem. 10, 359-384, 1991
A;Title: Heparad motifs within the distal subdomain of the coiled-coil rod region of M ph
A;Reference number: A44643; MUID:92143933; PMID:1781883
A;Accession: A44643
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-501 <MAN>
A;Experimental source: type M57, Strain A935
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIP:83737), NCBIP:83738!
A;Note: parts of this sequence were confirmed by peptide sequencing
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Maser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in *emm* gene sequences and the *pop*
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60833
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 14-95 <WHA>
A;Cross References: EMBL:U11971
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
C;Superfamily: M5 protein
C;Keywords: coiled coil; dimer

Query Match 100.0%; Score 64; DB 2; Length 501;
Best Local Similarity 100.0%; Pred. No. 0.025; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 12

S57835 IgG-binding protein emm1 precursor - *Streptococcus pyogenes* (strain 64/14)
A;Variety: IgG-binding protein type IIA; type IIA immunoglobulin G-binding prote
C;Species: *Streptococcus pyogenes*
C;Accession: S57835; S60931
C;Date: 28-Nov-1995 #sequence_revision 09-Mar-1996 #text_change 09-Jul-2004
R;Boyle, M.D.P.; Hawlitzky, J.; Raeder, R.; Podbielski, A.

Infect. Immun. 62, 1336-1347, 1994
A;Title: Analysis of genes encoding two unique type IIA immunoglobulin G-binding protein
A;Reference number: S57834; MUID:94178942; PMID:8132341
A;Accession: S57835
A;Molecule type: DNA
A;Residues: 1-528
A;Cross references: UNIPROT:Q54843; EMBL:X72932
A;Experimental source: strain 64/14
A;Note: the authors translated the codons CTAAA for residue 52 and 53 as Arg
R;Podbielski, A.
submitted to the EMBL Data Library, March 1993
A;Reference number: S58931
A;Accession: S58931
A;Molecule type: DNA
A;Residues: 1-46, E, 48-52, 'E', 54-528
A;Cross references: EMBL:X72932; NID:9507128; PIDN:CAA51437.1; PID:9507130
A;Experimental source: strain 64/14
C;Genetics:
A;Gene: emm1
C;Superfamily: M5 protein
F;-41/Domain: Signal sequence #status predicted <SIG>
F;42-528/Product: type IIA immunoglobulin G-binding protein emm1 #status predicted <SIG>
Query Match 100.0%; Score 64; DB 2; Length 528;
Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
Db 379 ASREAKKQVEKALE 392

RESULT 13

S54871 M protein - *Streptococcus* sp.
C;Species: *Streptococcus* sp.
C;Accession: S54871
R;Podbielski, A.; Melzer, B.
submitted to the EMBL Data Library, June 1991
A;Reference number: S54871
A;Accession: S54871
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-532 <POD>
A;Cross references: UNIPROT:Q55098; EMBL:X60097; NID:9840905; PIDN:CAA42693.1; PID:9840949
C;Superfamily: M5 protein

Query Match 100.0%; Score 64; DB 2; Length 532;
Best Local Similarity 100.0%; Pred. No. 0.026; Mismatches 0; Indels 0; Gaps 0;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ASREAKKQVEKALE 14
Db 383 ASREAKKQVEKALE 396

RESULT 14

A28549 M24 protein precursor - *Streptococcus pyogenes*
C;Species: *Streptococcus* Pyogenes
A;Variety: serotype M24
C;Accession: A28549; S60802
R;Mouw, A.R.; Beachey, E.H.; Burdett, V.
J; Bacteriol. 170, 676-684, 1988
A;Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence
A;Reference number: S8815166; PMID:3276655
A;Accession: A28549
A;Molecule type: DNA
A;Residues: 1-539 <MOU>
A;Cross references: UNIPROT:P12379; GB:MA19031; NID:9153616; PIDN:CAA26874.1; PID:9153617
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Maser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:891551
A;Accession: S60802
A;Species: Streptococcus pyogenes
A;Molecule type: DNA
A;Residues: 30-89 <WHA>
C;Superfamily: M5 protein
C;Keywords: coiled coil; transmembrane protein

Query Match 100.0%; Score 64; DB 2; Length 564;
Best Local Similarity 100.0%; Pred. No. 0.027;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ASREARKQVEKALE 14
Db 427 ASREARKQVEKALE 440

Search completed: August 4, 2005, 09:04:10
Job time : 16.3023 secs

Qy 1 ASREARKQVEKALE 14
Db 390 ASREARKQVEKALE 403

RESULT 15
A60115
M: Protein Precursor - Streptococcus pyogenes (serotype M12) (fragment)
C:Species: Streptococcus pyogenes
A;Variety: Serotype M12
C;Date: 08-Dec-1992 #sequence revision 08-Dec-1992 #text_change 09-Jul-2004
C;Accession: A40174; A60115; S39887; S60172; S60193
R;Robbins, J.C.; Spanier, J.G.; Jones, S.J.; Simpson, W.J.; Cleary, P.P.
J: Bacteriol. 169 5633-5640, 1987
A;Title: Streptococcus pyogenes type 12 M protein gene regulation by upstream sequences.
A;Reference number: A40174; MUID:88058777; PMID:2445730
A;Accession: A40174
A;Status: Translation not shown
A;Molecule type: DNA
A;Residues: 1-564 <ROB>
A;Cross-references: UNIPROT:P19401; GB:M18269; NID:g153543; PID:AAA88573_1; PID:g153544
R;Kraus, W.; Seyer, J.M.; Beachey, E.H.
Infec. Immun. 57, 2457-2461, 1989
A;Title: Vimentin-cross-reactive epitope of type 12 streptococcal M protein.
A;Reference number: A60115; MUID:89307564; PMID:2473037
A;Accession: A60115
A;Molecule type: protein
A;Residues: 42-54 <KRA>
R;Chen, C.; Bormann, N.; Cleary, P.P.
Mol. Gen. Genet. 241, 685-693, 1993
A;Title: VirR and Mry are homologous trans-acting regulators of M protein and C5a peptidase genes.
A;Reference number: S39886; MUID:94088463; PMID:7505399
A;Accession: S39887
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-15 <CHE>
R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
Submitted to the ENBL Data Library, July 1994
A;Description: Noncongruent relationships between variation in emm1 gene sequences and t
A;Reference number: S61072
A;Accession: S61072
A;Molecule type: DNA
A;Residues: 1-111 <WHA>
A;Cross-references: EMBL:U11337; NID:g533551; PID:AAA99533_1; PID:g1235807
R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
Mol. Microbiol. 14, 619-631, 1994
A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
A;Reference number: S60784; MUID:95198537; PMID:7891551
A;Accession: S60793
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 29-89 <WHW>
A;Cross-references: EMBL:U11937
C;Genetics:
A;Gene: emm12
C;Superfamily: M5 protein
C;Keywords: transmembrane protein
F;1-41/Domain: signal sequence #status predicted <SIG>
F;42-564/Product: M protein (fragment) #status predicted <MAT>

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OX "Genetic diversity and relationships among *Streptococcus* pyogenes strains expressing serotype M1 protein: recent intercontinental spread of a subclone causing episodes of invasive disease.";

RX Infect. Immun. 63:994-1003(1995).

DR EMBL; U20104; AAA85117.1; -.

DR HSSP; P13.6; IEA.

GO; GO:0016020; C:membrane; IEA.

InterPro; IPR003345; M_repeat.

DR Pfam; PF02370; M_1; -.

FT NON_TER 1 1

FT NON_TER 100 100

SQ SEQUENCE 100 AA; 11287 MW; 9773331914EDC2D3 CRC64;

Query Match Score 64; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.041; 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0;

Db 50 ASREAKKQVEKALE 63

RESULT 3

ID Q933A1 PRELIMINARY; PRT; 100 AA.

AC ORF3A1; -.

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)

DS M1_protein (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus

OX NCBI_TaxID=1314;

RN SEQUENCE FROM N A.

RX MEDLINE:95172752; PubMed=7868273;

RA Musser J.M., Kapoor V., Szeto J., Pan X., Swanson D.S., Martin D.R.;

RT "Genetic diversity and relationships among *Streptococcus* pyogenes strains expressing serotype M1 protein: recent intercontinental spread of a subclone causing episodes of invasive disease.";

RX Infect. Immun. 63:994-1003(1995).

DR EMBL; U20102; AAA85115.1; -.

DR HSSP; P13.6; IEA.

GO; GO:0016020; C:membrane; IEA.

InterPro; IPR003345; M_repeat.

DR Pfam; PF02370; M_1; -.

FT NON_TER 1 1

FT NON_TER 100 100

SQ SEQUENCE 100 AA; 11345 MW; 9773331C00EDC2D3 CRC64;

Query Match Score 64; DB 2; Length 100;

Best Local Similarity 100.0%; Pred. No. 0.041; 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0;

Db 50 ASREAKKQVEKALE 63

RESULT 4

ID Q54832 PRELIMINARY; PRT; 198 AA.

AC Q54832; -.

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE M_protein (Fragment).

DE Name=emm3;

GN Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus

OX NCBI_TaxID=1314;

RN [1] SEQUENCE FROM N A.

RC STRAIN=3-3/317;

RC MEDLINE=93062420; PubMed=14355517;

RA Podbielski A.; Baird R.; Kaufhold A.;

RT "The group A streptococcal M-type 3 protein gene exhibits a C terminus typical for class I M proteins";

RT Med. Microbiol. Immunol. 181:209-213(1992).

RN [2]

RP SEQUENCE FROM N A.

RC STRAIN=3-3/317;

RA Podbielski A.; Kaufhold A.;

RT Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

EMBL; X66816; CRA4729.1; -.

DR GO; GO:000986; C:cell surface; IEA.

DR GO; GO:000518; C:cell wall; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR001899; Gram_Pos_anchor.

DR InterPro; IPR003345; M_repeat.

DR Pfam; PF00746; Gram_pos_anchor; 1.

DR Prints; PRO0015; GPOSANCHOR.

DR TIGRFAMS; TIGR01167; LPXTG anchor; 1.

DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.

KW Cell wall; Peptidoglycan-anchor.

FT NON_TER 1 1

SQ SEQUENCE 198 AA; 21550 MW; A738888D94715SD5 CRC64;

Query Match Score 100.0%; Score 64; DB 2; Length 198;

Best Local Similarity 100.0%; Pred. No. 0.078; Mismatches 0; Indels 0; Gaps 0;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1 ASREAKKQVEKALE 14

Db 49 ASREAKKQVEKALE 62

RESULT 5

ID P95824 PRELIMINARY; PRT; 208 AA.

AC P95824; -.

DT 01-MAY-1997 (TREMBLrel. 03, Created)

DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)

DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)

DE M_protein (Fragment).

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus

OX NCBI_TaxID=1314;

RN [1] SEQUENCE FROM N A.

RC STRAIN=M nontypeable group A;

RC Brandt B.R.; Good M.R.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).

DR GO; GO:000986; C:cell surface; IEA.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR001899; Gram_Pos_anchor.

DR InterPro; IPR003345; M_repeat.

DR Prints; PRO0015; GPOSANCHOR.

DR TIGRFAMS; TIGR01167; LPXTG anchor; 1.

KW Cell wall; Peptidoglycan-anchor.

FT NON_TER 1 1

FT NON_TER 208 208

SY	SEQUENCE	208 AA;	22695 MW;	013FBABA0A97FF42 CRC64;	
	Query Match	100.0% ; Score 64 ; DB 2 ; Length 208;			
	Best Local Similarity	100.0% ; Pred. No. 0.082 ; Indels 0 ; Gaps 0 ;			
	Matches 14 ; Conservative 0 ; Mismatches 0 ;				
Qy		1 ASREAKKQVEKALE 14			
Db		59 ASREAKKQVEKALE 72			
RESULT 6					
P95825	ID	PRELIMINARY;	PRT;	208 AA.	
P95825;	AC				
DT 01-MAY-1997 (TrEMBLrel. 03, Created)	DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)				
M protein (Fragment).					
OS Streptococcus pyogenes					
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;					
OC Streptococcus					
OX NCBI_TaxID=1314;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=reference;					
RA Brandt E.R., Good M.F.;					
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.					
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).					
DR U65900; AAB0641_1;					
DR GO:0005986; C:cell surface; IEA.					
DR GO:0005618; C:cell wall; IEA.					
DR GO:0016020; C:membrane; IEA.					
DR InterPro; IPR001899; Gram_pos_anchor.					
DR InterPro; IPR003345; M_repeat.					
DR Pfam; PF00746; Gram_pos_anchor; 1.					
DR PRINTS; PR00015; GPSANCHOR.					
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.					
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.					
KW Cell wall; Peptidoglycan-anchor.					
FT 1	FT				
NON-TER 208	NON-TER 208				
SQ SEQUENCE 208 AA; 22695 MW;	SEQUENCE 208 AA; 22695 MW;	Query Match	Score 64 ; DB 2 ; Length 208;		
		Best Local Similarity	100.0% ; Pred. No. 0.082 ;		
		Mismatches 14 ;	Conservative 0 ; Mismatches 0 ;	Indels 0 ; Gaps 0 ;	
Qy		1 ASREAKKQVEKALE 14			
Db		59 ASREAKKQVEKALE 72			
RESULT 7					
P95826	ID	PRELIMINARY;	PRT;	208 AA.	
P95826;	AC				
DT 01-MAY-1997 (TrEMBLrel. 03, Created)	DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)				
M protein (Fragment).					
OS Streptococcus pyogenes					
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;					
OC Streptococcus					
OX NCBI_TaxID=1314;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=RHD152_;					
RA Brandt E.R., Good M.F.;					
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.					
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by					
an amide bond (By similarity).					
DR GO:0005986; C:cell surface; IEA.					
DR GO:0005618; C:membrane; IEA.					
DR InterPro; IPR003345; M_repeat.					
DR Pfam; PF00746; Gram_pos_anchor; 1.					
DR PRINTS; PR00015; GPSANCHOR.					
DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1.					
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.					
KW Cell wall; Peptidoglycan-anchor.					
FT 1	FT				
NON-TER 208	NON-TER 208				
SQ SEQUENCE 208 AA; 22817 MW;	SEQUENCE 208 AA; 22817 MW;	Query Match	Score 64 ; DB 2 ; Length 208;		
		Best Local Similarity	100.0% ; Pred. No. 0.082 ;		
		Mismatches 14 ;	Conservative 0 ; Mismatches 0 ;	Indels 0 ; Gaps 0 ;	
Qy		1 ASREAKKQVEKALE 14			
Db		59 ASREAKKQVEKALE 72			
RESULT 8					
Q84DD3	ID	PRELIMINARY;	PRT;	212 AA.	
Q84DD3;	AC				
DT 01-JUN-2003 (TrEMBLrel. 24, Created)	DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)				
DR GO:0005986; C:membrane; IEA.	DR GO:0005986; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR003345; M_repeat.	DR InterPro; IPR003345; M_repeat.				
DR Pfam; PF02370; M. 1.	DR Pfam; PF02370; M. 1.				
DR Q6TUR5; Q6TUR5	DR Q6TUR5; Q6TUR5				
DR GO:0016030; C:membrane; IEA.	DR GO:0016030; C:membrane; IEA.				
DR InterPro; IPR00334					

OX	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
RN	[1] NCBI_TaxID=1314;
RP	SEQUENCE FROM N.A.
RC	STRAIN=NS24;
RX	MEDLINE=22894607; PubMed=14532198;
RA	Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I., Ravins M., Koreman Z., Cohen-Poradosu R., Nir-Paz R.;
RT	"emm typing of M nontypeable invasive group A streptococcal isolates in Israel."
RL	J. Clin. Microbiol. 41:4655-4659 (2003).
DR	EMBL:AY394338; AAQ94330..1; -;
DR	GO:0016020; C:membrane; IEA.
DR	InterPro:IPR003345; M_repeat.
PFAM	PF02370; M; 1.
FT	NON-TER 1 1
FT	NON-TER 237 237
SQ	SEQUENCE 237 AA; 27027 MW; 47CFFF315DD4EB5F2 CRC64;
Query Match	Score 64; DB 2; Length 237;
Best Local Similarity	100.0%; Pred. No. 0.093;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ASREAKKOVEKALE 14
Db	192 ASREAKKOVEKALE 205
RESULT 10	Q6V9Q3 PRELIMINARY; PRT; 251 AA.
ID	Q6V9Q3
AC	Q6V9Q3;
DT	05-JUL-2004 (TREMBLrel. 27, Created)
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE	M protein (Fragment).
GN	Name=emm;
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
QC	Streptococcus pyogenes.
NCBI_TaxID	1314;
RN	[1] NCBI_TaxID=1314;
RP	SEQUENCE FROM N.A.
RC	STRAIN=JS8;
RA	Moses A.E., Hidalgo-Grass C., Dan-Goor M., Jaffe J., Shetzigovsky I., Ravins M., Koreman Z., Cohen-Poradosu R., Nir-Paz R.;
RL	Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR	EMBL:AY346386; AAQ73006..1; -;
DR	GO:0016020; C:membrane; IEA.
DR	InterPro:IPR003345; M_repeat.
PFAM	PF02370; M; 1.
FT	NON-TER 1 1
FT	NON-TER 251 251
SQ	SEQUENCE 251 AA; 28938 MW; 2A66602AAA637D11 CRC64;
Query Match	Score 64; DB 2; Length 251;
Best Local Similarity	100.0%; Pred. No. 0.098;
Matches	14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 ASREAKKOVEKALE 14
Db	221 ASREAKKOVEKALE 234
RESULT 11	Q8GL98 PRELIMINARY; PRT; 303 AA.
ID	Q8GL98
AC	Q8GL98;
DT	01-MAR-2003 (TREMBLrel. 23, Created)
DT	01-MAR-2004 (TREMBLrel. 23, Last sequence update)
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE	M protein (Fragment).
GN	Name=emm;
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID	1314;
OX	

[1] RN SEQUENCE FROM N.A. Krejany S., Srivakash K.S., Delvecchio A.,
 RA Dyall-Smith M.L., Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 RA McMillan D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY139409; AAN64682.1; -.
 DR GO:GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003345; M_repeat.
 DR Pfam; PF02370; M; 2.
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 303 AA; 303 MW; F76F37540E16CD1B CRC64;
 Query Match 100.0%; Score 64; DB 2; Length 303;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASREAKKQVEKALE 14
 Db 246 ASREAKKQVEKALE 259
 Search completed: August 4, 2005, 09:03:17
 Job time : 76.2326 secs

RESULT 14
 Q8GL84 PRELIMINARY; PRT; 307 AA.
 ID Q8GL84;
 AC Q8GL84;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE M protein (Fragment).
 GN Name-emm;
 OS Streptococcus pyogenes;
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Dyall-Smith M.L., Krejany S., Srivakash K.S., Delvecchio A.,
 RA McMillan D.;
 RL Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AY139423; AAN64696.1; -.
 DR GO:GO:0016020; C:membrane; IEA.
 DR InterPro; IPR003345; M_repeat.
 DR Pfam; PF02370; M; 2.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 307 AA; 34955 MW; 2268229938E66E0E CRC64;
 Query Match 100.0%; Score 64; DB 2; Length 307;
 Best Local Similarity 100.0%; Pred. No. 0.12;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 ASREAKKQVEKALE 14
 Db 251 ASREAKKQVEKALE 264
 Search completed: August 4, 2005, 09:03:17
 Job time : 76.2326 secs

RESULT 15
 Q8GL80 PRELIMINARY; PRT; 314 AA.
 ID Q8GL80;
 AC Q8GL80;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DE M protein (Fragment).
 GN Name-emm;
 OS Streptococcus pyogenes;
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus;
 NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A. Krejany S., Srivakash K.S., Delvecchio A.,
 RA

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(c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 4, 2005, 08:37:33 ; Search time 163.209 Seconds
(without alignments)
68.722 Million cell updates/sec

Title: US-10-706-275-2
Perfect score: 137
Sequence: 1 KQAEKDKVKASREAKKQVEKALEQLEDKVK 29

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0\$
Maximum Match 100\$
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqP1980s:*
- 2: geneseqP1990s:*
- 3: geneseqP2000s:*
- 4: geneseqP2001s:*
- 5: geneseqP2002s:*
- 6: geneseqP2003s:*
- 7: geneseqP2003s:*
- 8: geneseqP2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	137	100.0	29	8	ADK00565	Ad00565 Immunogen
2	137	100.0	45	8	ADK00571	Ad00571 Immunogen
3	137	100.0	46	8	ADK00569	Ad00569 Immunogen
4	137	100.0	46	8	ADK00572	Ad00572 Immunogen
5	137	100.0	47	8	ADK00570	Ad00570 Immunogen
6	125	91.2	28	2	AAW04353	Aaw04353 ChimERIC
7	123	89.8	28	2	AAW04354	Aaw04354 ChimERIC
8	116	84.7	28	2	AAW04355	Aaw04355 ChimERIC
9	110	80.3	28	2	AAW04352	Aaw04352 ChimERIC
10	96	70.1	28	2	AAW04351	Aaw04351 ChimERIC
11	81	59.1	28	2	AAW04350	Aaw04350 ChimERIC
12	78	56.9	28	2	AAR97454	Aar97454 ChimERIC
13	72	52.6	234	2	AAR10221	Streptoco
14	72	52.6	281	2	AAR20128	Sequence
15	72	52.6	441	1	AAP90955	M6 strept
16	72	52.6	441	2	AAR1780	Streptoco
17	72	52.6	441	7	ADG62862	Streptoco
18	72	52.6	483	2	AAW08927	Type-6 M-
19	72	52.6	484	5	ABP30015	Streptoco
20	72	52.6	484	8	ADR81969	S. Pyogen
21	71	51.8	28	2	AAR97396	(Gen4) 4 a
22	71	51.8	236	3	AAB03118	C-terminal
23	71	51.8	254	2	AAR50228	Sequence
24	71	51.8	284	2	AAR50229	Sequence
25	71	51.8	305	2	AAR50996	Recombina

ALIGNMENTS

RESULT 1
ADK00565
ID ADK00565 standard; peptide; 29 AA.
XX
AC
XX
DT 06-MAY-2004 (first entry)

XX
DE Immunogenic lipopeptide of the invention #101.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antilulcer;
KW Antinfertility; Vaccine; antibody.
XX
OS Synthetic.
XX
PN WO2004014956-A1.
XX
PD 19-FEB-2004.
XX
PF 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0102838P.
XX
PA (COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX
DR WPT; 2004-218735/22.

SUMMARIES

#	Query	Match	Length	DB ID	Description
1	Ad00565 Immunogen	Ad00565 Immunogen	29	8	ADK00565
2	Ad00571 Immunogen	Ad00571 Immunogen	45	8	ADK00571
3	Ad00569 Immunogen	Ad00569 Immunogen	46	8	ADK00569
4	Ad00572 Immunogen	Ad00572 Immunogen	47	8	ADK00572
5	Ad00570 Immunogen	Ad00570 Immunogen	47	8	ADK00570
6	Aaw04353 ChimERIC	Aaw04353 ChimERIC	91.2	28	AAW04353
7	Aaw04354 ChimERIC	Aaw04354 ChimERIC	89.8	28	AAW04354
8	Aaw04355 ChimERIC	Aaw04355 ChimERIC	84.7	28	AAW04355
9	Aaw04352 ChimERIC	Aaw04352 ChimERIC	80.3	28	AAW04352
10	Aaw04351 ChimERIC	Aaw04351 ChimERIC	70.1	28	AAW04351
11	Aaw04350 ChimERIC	Aaw04350 ChimERIC	59.1	28	AAW04350
12	Aar97454 ChimERIC	Aar97454 ChimERIC	56.9	28	AAR97454
13	AAR10221 Streptoco	AAR10221 Streptoco	52.6	234	AAR10221
14	AAR20128 Sequence	AAR20128 Sequence	52.6	281	AAR20128
15	AAP90955 M6 strept	AAP90955 M6 strept	52.6	441	AAP90955
16	Streptoco	Streptoco	52.6	441	AAR1780
17	Streptoco	Streptoco	52.6	441	ADG62862
18	AAW08927 Type-6 M-	AAW08927 Type-6 M-	52.6	483	AAW08927
19	ABP30015 Streptoco	ABP30015 Streptoco	52.6	484	ABP30015
20	S. Pyogen	S. Pyogen	52.6	484	ADR81969
21	(Gen4) 4 a	(Gen4) 4 a	51.8	28	AAR97396
22	C-terminal	C-terminal	51.8	236	AAB03118
23	Sequence	Sequence	51.8	254	AAR50228
24	Sequence	Sequence	51.8	284	AAR50229
25	Recombina	Recombina	51.8	305	AAR50996

CC
The present invention relates to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid sequences of T helper cell epitope and B cell epitope, where amino acid sequences are different, and internal lysine residues or internal lysine analog residues for covalent attachment of each of lipid moieties through CC
Kegg; amino group or terminal side chain group of lysine or lysine analog. The Peptides are useful in eliciting immune response against group A Streptococcus PT
PT useful for eliciting immune response against group A Streptococcus PT antigen. PT
CC
Claim 29: SEQ ID NO 101; 194pp; English.

CC
The present invention relates to a lipopeptide comprising polypeptide conjugated to lipid moieties, where polypeptide contains amino acid CC
sequences of T helper cell epitope and B cell epitope, where amino acid CC
sequences are different, and internal lysine residues or internal lysine CC
analog residues for covalent attachment of each of lipid moieties through CC
Kegg; amino group or terminal side chain group of lysine or lysine CC
analog. The Peptides are useful in eliciting the production of antibody CC
against an antigenic B cell epitope in a subject, and are useful for CC
antibody production, synthetic vaccine production, diagnostic method CC
employing antibodies and antibody ligands and immunotherapy for CC
veterinary and human medicine. The method efficiently elicits the CC
production of antibody against antigenic B cell epitope. The present CC

CC sequence represents a novel immunogenic lipopeptide comprising T helper
CC and B cell epitopes.
XX

SQ Sequence 29 AA;

Query Match 100.0%; Score 137; DB 8; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.1e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQAEDKVKA\$REAKQVEKAL\$OLEQEDVK 29

Db 1 KQAEDKVKA\$REAKQVEKAL\$OLEQEDVK 29

RESULT 2
ADK00571
ID ADK00571 standard; peptide: 45 AA.
XX

AC ADK00571;
XX
DT 06-MAY-2004 (first entry)
XX

DE Immunogenic lipopeptide of the invention #107.
XX
KW T helper cell epitope; B cell epitope; Antibacterial; Antiulcer;
XX
KW Antiinfectivity; Vaccine; antibody.
XX

OS Synthetic.
XX
PA WO2004014956-A1.
XX
PD 19-FEB-2004.
XX

PN WO2004014956-A1.
XX
PR 19-FEB-2004.
XX

XX
PP 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0402838P.
XX

XX
PS (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX
DR WPI: 2004-238735/22.
XX

XX
PP 12-AUG-2003; 2003WO-AU001018.
XX
PR 12-AUG-2002; 2002US-0402838P.
XX

XX
PS (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
XX
PI Jackson D, Zeng W;
XX
DR WPI: 2004-238735/22.
XX

XX
PR Novel lipopeptide comprising polypeptide having amino acid sequence of T
helper cell epitope and B cell epitope, conjugated to lipid moieties,
useful for eliciting immune response against group A Streptococcus
antigen.
XX
PS Claim 39; SEQ ID NO 105; 194pp; English.
XX

XX
The present invention relates to a lipopeptide comprising polypeptide
conjugated to lipid moieties, where polypeptide contains amino acid
sequence of T helper cell epitope and B cell epitope, where amino acid
sequences are different, and internal lysine residues or internal lysine
analog residues for covalent attachment of each of lipid moieties through
CC amino group or terminal side chain group of lysine or lysine
analog. The peptides are useful in eliciting the production of antibody
against an antigenic B cell epitope in a subject, and are useful for
CC antibody production, synthetic vaccine production, diagnostic method
CC employing antibodies and antibody ligands and immunotherapy for
veterinary and human medicine. The method efficiently elicits the
CC production of antibody against antigenic B cell epitope. The present
CC sequence represents a novel immunogenic lipopeptide comprising T helper
CC and B cell epitopes.
XX
SQ Sequence 45 AA;

Query Match 100.0%; Score 137; DB 8; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.9e-09;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KQAEDKVKA\$REAKQVEKAL\$OLEQEDVK 29

Db 18 KQAEDKVKA\$REAKQVEKAL\$OLEQEDVK 46

RESULT 4
ADK00572
ID ADK00572 standard; peptide: 46 AA.
XX
AC ADK00572;
XX
DT 06-MAY-2004 (first entry)
XX
Qy 1 KQAEDKVKA\$REAKQVEKAL\$OLEQEDVK 29

PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
 PA (UWME) UNIV MELBOURNE.
 PA HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX
 PI Cooper JA, Relef WA, Good MF, Saul AJ;
 XX DR WPI: 1996-221939/22.
 XX
 PT New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 PS Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimeric peptide (CP) contg. the Streptococcal
 M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 (1992)). The CP comprises a B-cell conformational epitope from within
 p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 the GCN4 leucine zipper Peptide (AAR97395). The 2nd peptide has a similar
 conformation, enabling the epitope to be presented in an immunologically
 active conformation. The CP can be used in a novel detection/mapping
 process, e.g. to determine the min. epitope required to induce opionic
 antibodies (Ab), and in vaccines against gp. A Streptococci Ab raised
 against the CP can be used for immunotherapy and diagnosis, while the CP
 peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match 91.2%; Score 125; DB 2; Length 28;
 Best Local Similarity 92.9%; Prod. No. 3e-08; Indels 0; Gaps 0;
 Matches 26; Conservative 2; Mismatches 0; Delins 0; Indels 0; Gaps 0;
 Qy 1 KQABDKVKAASREAKKQVEKALEQEDVKY 28
 Db 1 KQABDKVKAASREAKKQVEKALEQEDVKY 28

RESULT 7
 AAW04354 Standard; protein; 28 AA.
 ID AAW04354
 XX AC AAW04355;
 XX DT 02-DEC-1996 (first entry)
 XX DE Chimaeric peptide (J8) contg. Streptococcal M protein peptide p145.
 XX DE Chimaeric peptide (J8) contg. Streptococcal M protein peptide p145.
 XX DE Chimaeric peptide; M protein; peptide; p145; chimaeric; B-cell;
 KW Streptococcal; M protein; peptide; p145; chimaeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opionic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 XX OS Synthetic.
 XX FH Location/Qualifiers
 FT 16..27 /note= "p145 conformational B-cell epitope"
 FT XX EN W09611944-A1.
 XX PD 25-APR-1996.
 XX PR 16-OCT-1995; 95WO-AU000681.
 XX PR 14-OCT-1994; 94AU-00008851.
 XX PR (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX PR (UWME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.

PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX PI Cooper JA, Relef WA, Good MF, Saul AJ;
 XX DR WPI: 1996-221939/22.
 XX
 PT New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 PS Example 12; Fig 1C; 99pp; English.
 XX
 CC The present peptide is a chimeric peptide (CP) contg. the Streptococcal
 M Protein Peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 (1992)). The CP comprises a B-cell conformational epitope from within
 p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 the GCN4 leucine zipper Peptide (AAR97395). The 2nd peptide has a similar
 conformation, enabling the epitope to be presented in an immunologically
 active conformation. The CP can be used in a novel detection/mapping
 process, e.g. to determine the min. epitope required to induce opionic
 antibodies (Ab), and in vaccines against gp. A Streptococci Ab raised
 against the CP can be used for immunotherapy and diagnosis, while the CP
 peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match 89.8%; Score 123; DB 2; Length 28;
 Best Local Similarity 92.9%; Prod. No. 5.3e-08;
 Matches 26; Conservative 1; Mismatches 1; Delins 0; Indels 0; Gaps 0;
 Qy 2 QAEQDKVKAASREAKKQVEKALEQEDVKY 29
 Db 1 QAEQDKVKAASREAKKQVEKALEQEDVKY 28

RESULT 8
 AAW04355 Standard; protein; 28 AA.
 ID AAW04355
 XX AC AAW04355;
 XX DT 02-DEC-1996 (first entry)
 XX DE Chimaeric peptide (J9) contg. Streptococcal M protein peptide p145.
 XX KW Streptococcal; M protein; peptide; p145; chimaeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opionic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 XX OS Synthetic.
 XX FH Location/Qualifiers
 FT 17..28 /note= "p145 conformational B-cell epitope"
 FT XX EN W09611944-A1.
 XX PD 25-APR-1996.
 XX PR 16-OCT-1995; 95WO-AU000681.
 XX PR 14-OCT-1994; 94AU-00008851.
 XX PR (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PR (CSIR) COMMONWEALTH SCI & IND RES ORG.
 XX PR (UWME) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.

PA (CSLC-) CSL LTD.
 XX Cooper JA, Relf WA, Good MF, Saul AJ;
 PI WPI; 1996-221939/22.
 XX
 PT New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 PS Example 12; FIG 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation, enabling the epitope to be presented in a novel detection/mapping
 CC process, e.g. to determine the man. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match Score 116; DB 2; Length 28;
 Best Local Similarity 92.6%; Pred. No. 3.7e-07;
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 3 AEDKVTKASREAKQVEKAKVQEQLEDKVK 29
 Db 1 AEDKVTKQLEAKQVEKAKVQEQLEDKVK 27

RESULT 9
 ID AAW04352 standard; protein; 28 AA.
 XX AC AAW04352;
 XX DT 02-DEC-1996 (first entry)
 XX Chimaeric peptide (J5) contg. Streptococcal M protein peptide p145.
 DE Streptococcal; M protein; peptide; p145; chimaeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 14 :25 /note= "p145 conformational B-cell epitope"
 FT Peptide 14 :25 /note= "p145 conformational B-cell epitope"
 FT PN WO9611944-A1.
 XX PD 25-APR-1996.
 XX PF 16-OCT-1995; 95WO-AU000681.
 XX PR 16-OCT-1995; 95AU-00008851.
 XX PR 14-OCT-1994; 94AU-00008851.
 XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PA (CSR) COMMONWEALTH SCI & IND RES ORG.
 PA (UTME) UNIV MELBOURNE
 PA (HALL) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX

PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX DR WPI; 1996-221939/22.
 XX PT New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX
 PS Example 12; FIG 1C; 99pp; English.
 XX
 CC The present peptide is a chimaeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Pruksakorn et al, J. Immunol. 149: 2729-2735
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (AAR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the man. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX
 SQ Sequence 28 AA;
 Query Match Score 110; DB 2; Length 28;
 Best Local Similarity 85.2%; Pred. No. 2e-06;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KQADBKVKAASREAKQVEKAKVQEQLEDKVK 27
 Db 2 KQADBKVDAASREAKQVEKAKVQEQLEDKVK 28

RESULT 10
 ID AAW04351
 XX AC AAW04351 standard; protein; 28 AA.
 XX DT 02-DEC-1996 (first entry)
 XX DE Chimaeric peptide (J5) contg. Streptococcal M protein peptide p145.
 XX KW Streptococcal; M protein; peptide; p145; chimaeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; group A Streptococci; immunotherapy;
 KW diagnosis.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH 13 :24 /note= "p145 conformational B-cell epitope"
 FT Peptide 13 :24 /note= "p145 conformational B-cell epitope"
 FT PN WO9611944-A1.
 XX PD 25-APR-1996.
 XX PF 16-OCT-1995; 95WO-AU000681.
 XX PR 14-OCT-1994; 94AU-00008851.
 XX PA (COUN-) COUNCIL QUEENSLAND INST MEDICAL RES.
 XX PA (CSR) COMMONWEALTH SCI & IND RES ORG.
 PA (UTME) UNIV MELBOURNE
 PA (HALL) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 XX PI Cooper JA, Relf WA, Good MF, Saul AJ;

DR WPI; 1996-221939/22.
 XX New chimeric peptide(s) including a conformational epitope - inserted
 PT into a peptide having similar native conformation, useful in vaccines and
 PR for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX Example 12; Fig 1C; 99pp; English.

XX The present peptide is a chimeric peptide (CP) contg. the Streptococcal
 CC M protein peptide p145 (Pruksakorn et al., J. Immunol. 149: 2729-2735;
 CC (1992)). The CP comprises a B-cell conformational epitope from within
 CC p145, inserted into a 2nd peptide, pref. an alpha-helical coil based on
 CC the GCN4 leucine zipper peptide (ARR97395). The 2nd peptide has a similar
 CC conformation, enabling the epitope to be presented in an immunologically
 CC active conformation. The CP can be used in a novel detection/mapping
 CC process, e.g. to determine the min. epitope required to induce opsonic
 CC antibodies (Ab), and in vaccines against gp. A Streptococci. Ab raised
 CC against the CP can be used for immunotherapy and diagnosis, while the CP
 CC can be used diagnostically to detect Ab. The reactivity of the present
 CC peptide to the anti-p145 mouse serum 11/1(8) given as a mean absorbance
 CC value at 405 nm was ca. 0.2, compared to ca. 1.8 for p145
 XX SQ Sequence 28 AA;

Query	Match	Score	DB 2;	Length	28;
Best Local Similarity	96.9%	Pred. No.	9	Mismatches	0;
Matches 20;	Conservative	3;	Indels	0;	Gaps 0;

Qy 1 KQADEKVKRASREAKQVKEAKLEQED 26
 Db 3 KQADEKVKRASREAKQVKEAKLEQED 28

RESULT 11
 ARR97154 ID AAR97454 standard; peptide; 28 AA.
 XX AC AAR97454;
 XX DT 04-DEC-1996 (First entry)
 XX DB Chimeric peptide a986 contg. C. elegans unc-15 paramyosin Peptide.
 XX KW Paramyosin protein; peptide; unc-15; chimaeric; B-cell;
 KW conformational epitope; alpha-helix; GCN4; leucine zipper; detection;
 KW mapping; opsonic antibody; vaccine; immunotherapy; diagnosis.
 XX OS Synthetic.
 XX PN WO9611944-A1.
 XX PD 25-APR-1996.
 XX PF 16-OCT-1995; 95WO-AU000681.
 XX PR 14-OCT-1994; 94AU-00008851.
 PN WO9611944-A1.
 XX Key Location/Qualifiers
 FT 12..23 /note= "p145 conformational B-cell epitope"
 XX
 PR 25-APR-1996.
 XX 16-OCT-1995; 95WO-AU000681.
 XX 14-OCT-1994; 94AU-00008851.
 XX
 PA (COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIRO) COMMONWEALTH SCI & IND RES ORG.
 PA (TUMBLE) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 PA (CSLC-) CSL LTD.
 PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX WPI; 1996-221939/22.
 XX
 PR 25-APR-1996.
 XX 16-OCT-1995; 95WO-AU000681.
 XX 14-OCT-1994; 94AU-00008851.
 XX
 PA (COUNCIL QUEENSLAND INST MEDICAL RES.
 PA (CSIRO) COMMONWEALTH SCI & IND RES ORG.
 PA (TUMBLE) UNIV MELBOURNE.
 PA (HALL-) HALL INST MEDICAL RES WALTER & ELIZA.
 PA (BIOT-) BIOTECH AUSTRALIA PTY LTD.
 XX
 PI Cooper JA, Relf WA, Good MF, Saul AJ;
 XX WPI; 1996-221939/22.
 DR

PT New chimeric peptide(s) including a conformational epitope - inserted
 PR into a peptide having similar native conformation, useful in vaccines and
 PT for determin. of minimal epitope(s) or for mapping amphipathic helices.
 XX Example 12; Fig 1C; 99pp; English.

XX The present peptide is a chimaeric peptide (CP), contg. a C. elegans unc-

CC 15 paramyosin peptide. The CP comprises a B-cell conformational epitope
 CC from within unc-15, inserted into a 2nd peptide, pref. an alpha-helical
 CC coil based on the GCN4 leucine zipper Peptide (AAR97395). The 2nd Peptide
 CC has a similar conformation, enabling the epitope to be presented in an
 CC immunologically active conformation. The CP can be used in a novel
 CC detection/mapping process, e.g. to determine the min. epitope required to
 CC induce opsonic antibodies (Ab) and in vaccines against *C. elegans*. Ab
 CC raised against the CP can be used for immunotherapy and diagnosis, while
 CC the CP can be used diagnostically to detect Ab
 XX Sequence 28 AA;

Query Match Score 7B; DB 2; Length 28;
 Best Local Similarity 64.0%; Pred. No. 0.015; Gaps 0;
 Matches 16; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 1 KQAEQDKVKAQSREAKKQVEKALEQLE 25
 |||| : ||| : ; : :|||:
 DB 4 KQAEQDDLDAQSREAKKQLDQKVVKOLE 28

RESULT 13
 AAR10221 standard; protein; 234 AA.
 ID AAR10221
 XX
 AC AAR10221;
 XX
 DT 25-MAR-2003 (revised)
 DT 26-MAR-1991 (first entry)
 XX
 Streptococcal M6' protein.
 DE XX
 streptococcal M protein; M'6 protein; vaccinia virus; fowlpox virus;
 KW XX
 poxviridae vaccine; streptococcal pharyngitis.
 KW XX
 Streptococcus sp.
 OS XX
 WO9115872-A.
 OS XX
 PD 27-DEC-1990.
 XX
 PR 21-JUN-1989; 89US-00369118.
 XX
 PR 21-JUN-1989; 89US-00369118.
 PR 19-JUN-1990; 90US-00540586.
 XX
 PA (UYRQ) UNIV ROCKEFELLER.
 PA (OYOR-) UNIV OREGON STATE.
 XX
 PI Fischetti VA, Kruby DE;
 XX
 DR WPI: 1991-022236/03.
 DR N-PSDB; AAQ10244.
 XX
 PS New recombinant streptococcal M protein DNA and viral vector - for
 PR production of poxvirus vaccines in treatment of vaccinia, fowlpox etc.
 Disclosure: Fig 5; 41pp; English.

XX This M'6 protein corresponds to the conserved exposed polypeptide region
 CC of the streptococcal M protein. It is encoded by a genetically
 CC engineered gene introduced into the genome of a vaccinia or fowlpox
 CC virus. The resultant DNA complex is useful as a vaccine for
 CC immunoprotection against streptococcal infections. The M'6 polypeptide is
 CC the part of protein M responsible for virulence. (Updated on 25-MAR-2003
 CC to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)
 XX Sequence 234 AA;

Query Match Score 72; DB 2; Length 234;
 Best Local Similarity 45.2%; Pred. No. 0.81; Gaps 1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

QY 5 DRYK-----ASREAKKQVEKALEQLEQLEDKV 28
 Db 63 DRYKEEKQISDASSRQLRRDLDASREAKKQVEKALEBANSKL 104
 RESULT 14
 AAR20128
 ID AAR20128 standard; protein; 281 AA.
 XX
 AC AAR20128;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-APR-1992 (first entry)
 XX Sequence encoded by truncated M1 gene.
 XX Protein H; immunoglobulin G; IgG; antibody; autoimmune disease.
 XX Streptococcus sp.
 XX
 Location/Qualifiers
 FH Key 1..28
 FT Region /label= p16M1
 FT Region 29..70
 FT Region /label= C1
 FT Region 71..112
 FT Region /label= C2
 FT Region 113..155
 FT Region /label= C3
 FT Region 156..176
 FT Region /label= C4
 FT Region 177..281
 FT Region /label= D
 XX WO9119740-A.
 XX
 PD 26-DEC-1991.
 XX
 PF 21-JUN-1990; 90SE-00002212.
 XX
 PR 21-JUN-1990; 90SE-00002212.
 XX
 PA (HIGH-) HIGHTECH RECEPPOR A.
 XX
 PI Schmidt KH, Akesson P, Cooney J, Bjorck L;
 XX
 WPI; 1992-024366/03.
 DR N-PSDB; AAQ20292.
 XX
 PT New IgG binding protein H' lacking an albumin binding sequence - useful
 PT in purifinc. of excess IgG from blood and to diagnose autoimmune
 PT diseases.
 XX Disclosure: Fig 8; 37pp; English.
 XX
 CC The inventors claim a protein prod. by a strain of Gp.A Streptococci. The
 CC protein has the AA sequence of protein H but lacks at least some part of
 CC the C and D regions (responsible for binding albumin), esp. it lacks the
 CC whole of these regions and extends for AAI to AA158. Compared with
 CC natural protein H, it is more specific and may be used as part of a kit
 CC for the binding, separation and identification of human IgG. The same
 CC sequences appear in WO9119741. (Updated on 27-AUG-2003 to correct OS
 CC field.)
 XX Sequence 281 AA;
 Query Match Score 72; DB 2; Length 281;
 Best Local Similarity 45.2%; Pred. No. 0.99; Gaps 1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
 QY 5 DRYK-----ASREAKKQVEKALEQLEQLEDKV 28
 Db 110 DRYKEEKQISDASSRQLRRDLDASREAKKQVEKALEBANSKL 151

RESULT 15
 APP90955 ID AAP90955 standard; protein; 441 AA.
 XX AC AAP90955;
 XX DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 23-FEB-1990 (first entry)
 XX DE M6 streptococcal protein.

XX KW Immunoglobulin.
 XX OS Stretococcus sp; 'group A'.
 XX PS Location/Qualifiers

Key	Location/Qualifiers
FT Region	216..235
FT Region	248..269
FT Region	275..284

XX PN W08909064-A.
 XX PD 05-OCT-1989.
 XX PF 13-MAR-1989; 89WO-US001056.
 XX PR 25-MAR-1988; 88US-00173380.
 PR 27-FEB-1989; 89US-00315588.
 XX PA (UYRQ) UNIV ROCKEFELLER.
 XX PI Fischetti VA;
 XX DR 1989-309382/42.
 XX PT Polypeptide(s) from streptococcal M Protein - used to prepare vaccines
 PR for providing protection against streptococcal infection.
 XX Disclosure; Fig 1; 22pp; English.

XX The regions (pref. conjugated to a natural carrier, eg cholera toxin)
 CC above can elicit an immune Ig response in a mammal. They are used in
 CC vaccines against streptococcal infection, and give protection to
 CC different serotypes. (Updated on 25-MAR-2003 to correct PR field.)
 CC (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to
 CC correct PI field.) (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 441 AA;

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Query Match      52.6%; Score 72; DB 1; Length 441;
Best Local Similarity 45.2%; Prod: No. 1.6;
Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
Qy   5 DKVKG-----ASREAAKQVKPALEQDKV 28
Db 270 DKVKEEKQISDASRQGLRRDLDASREAKQVERALEEANSKL 311
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Search completed: August 4, 2005, 08:59:24
 Job time : 164.209 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 4, 2005, 08:27:17 ; Search time 40.4651 Seconds

(without alignments)

53.498 Million cell updates/sec

Title: US-10-706-275-2

Perfect score: 137

Sequence: 1 KQADKVKASREAKKQVEKALEQQLEDKVK 29

Scoring table: BLOSUM62

Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters:

513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
 1: /cggn2_6/ptodata/1/iaa/5A_COMB.pep:
 2: /cggn2_6/ptodata/1/iaa/5B_COMB.pep:
 3: /cggn2_6/ptodata/1/iaa/6A_COMB.pep:
 4: /cggn2_6/ptodata/1/iaa/6B_COMB.pep:
 5: /cggn2_6/ptodata/1/iaa/PCTUS.COM.pep:
 6: /cggn2_6/ptodata/1/iaa/backtiles.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	110	80.3	28	3	US-08-817-811-18	Sequence 18, Appl
2	96	70.1	28	3	US-08-811-811-17	Sequence 17, Appl
3	81	59.1	28	3	US-08-811-811-16	Sequence 16, Appl
4	78	56.9	28	3	US-08-811-811-67	Sequence 67, Appl
5	72	52.6	440	4	US-08-756E-35	Sequence 35, Appl
6	72	52.6	443	2	US-08-798-475-6	Sequence 6, Appl
7	72	52.6	433	4	US-08-278B-6	Sequence 6, Appl
8	71	51.8	438	3	US-08-811-811-12	Sequence 12, Appl
9	71	51.8	236	3	US-08-931-271-11	Sequence 11, Appl
10	71	51.8	254	4	US-08-914-479A-4	Sequence 4, Appl
11	71	51.8	284	4	US-08-914-479A-6	Sequence 6, Appl
12	71	51.8	305	3	US-08-931-271-10	Sequence 10, Appl
13	68.5	50.0	28	3	US-08-811-811-66	Sequence 66, Appl
14	67	48.9	29	3	US-08-811-811-52	Sequence 52, Appl
15	65.5	47.8	28	3	US-08-811-811-15	Sequence 15, Appl
16	65	47.4	29	3	US-08-811-811-74	Sequence 74, Appl
17	64	46.7	20	3	US-08-811-811-1	Sequence 1, Appl
18	64	46.7	29	3	US-08-811-811-73	Sequence 73, Appl
19	64	46.7	72	1	US-08-175A-87	Sequence 87, Appl
20	64	46.7	72	1	PCT-US92-06412-87	Sequence 87, Appl
21	64	46.7	361	4	US-09-541-A-5390	Sequence 5390, Ap
22	63	46.0	29	3	US-08-811-811-79	Sequence 1, Appl
23	63	46.0	107	1	US-08-175A-105	Sequence 105, Appl
24	63	46.0	107	1	US-08-474-633A-92	Sequence 92, Appl
25	63	46.0	107	4	US-08-823-771-92	Sequence 92, Appl
26	63	46.0	107	4	PCT-US92-06412-105	Sequence 105, Appl
27	62	45.3	28	3	US-08-811-811-13	Sequence 13, Appl

ALIGNMENTS

28	62	45.3	29	3	US-08-817-811-78	Sequence 78, Appl
29	62	45.3	77	1	US-08-474-633A-57	Sequence 57, Appl
30	62	45.3	77	1	US-08-474-633A-75	Sequence 75, Appl
31	62	45.3	77	4	US-08-823-771-75	Sequence 75, Appl
32	62	45.3	77	5	PCT-US92-06412-57	Sequence 75, Appl
33	61	44.5	28	1	US-08-175A-49	Sequence 49, Appl
34	61	44.5	28	1	US-08-474-633A-58	Sequence 58, Appl
35	61	44.5	28	4	US-08-823-771-58	Sequence 58, Appl
36	61	44.5	28	5	PCT-US92-06412-49	Sequence 49, Appl
37	61	44.5	29	3	US-08-817-811-71	Sequence 71, Appl
38	61	44.5	29	3	US-08-811-71-72	Sequence 72, Appl
39	61	44.5	29	3	US-08-817-811-75	Sequence 75, Appl
40	61	44.5	29	3	US-08-817-811-89	Sequence 89, Appl
41	61	44.5	37	1	US-08-175A-85	Sequence 97, Appl
42	61	44.5	37	1	US-08-474-633A-97	Sequence 85, Appl
43	61	44.5	37	1	US-08-474-633A-86	Sequence 86, Appl
44	61	44.5	37	4	US-08-823-771-85	Sequence 85, Appl

Qy 1 KQAEDKVKASREAKKKQVKALEQLEDK 27
 Db 2 KQAEDKLDSREAKKKQVKVQLEDK 28

RESULT 2
 US-08-811-17 Application US/08817811
 / Sequence No. 6174528
 / GENERAL INFORMATION:
 / APPLICANT: Cooper, Juan A.
 / APPLICANT: Relf, Wendy A.
 / APPLICANT: Good, Michael F.
 / APPLICANT: Saul, Allan J.
 / TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 / TITLE OF INVENTION: COMPRISING SAME
 / NUMBER OF SEQUENCES: 97
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Arnold, White & Durkee
 / STREET: P.O. Box 4433
 / CITY: Houston
 / STATE: Texas
 / COUNTRY: USA
 / ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: FBRC:005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-811-16

Query Match 59.1%; Score 81; DB 3; Length 28;
 Best Local Similarity 68.0%; Pred. No. 0.0035; Indels 0; Gaps 0;

Qy 1 KQAEDKVKAASREAKKKQVKALEQLED 25
 Db 4 KQAEDDLDASREAKKVQDKVKQLE 28

RESULT 4
 US-08-811-17 Application US/08817811
 / Sequence No. 6174528
 / GENERAL INFORMATION:
 / APPLICANT: Cooper, Juan A.
 / APPLICANT: Relf, Wendy A.
 / APPLICANT: Good, Michael F.
 / APPLICANT: Saul, Allan J.
 / TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 / TITLE OF INVENTION: COMPRISING SAME
 / NUMBER OF SEQUENCES: 97
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Arnold, White & Durkee
 / STREET: P.O. Box 4433
 / CITY: Houston
 / STATE: Texas
 / COUNTRY: USA
 / ZIP: 77210

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996

ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 67:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-811-67

Query Match 56.9%: Score 78; DB 3; Length 28;
 Best Local Similarity 64.0%; Pred. No. 0.0077; Gaps 0;
 Matches 16; Conservative 5; Mismatches 4; Indels 0;

Qy 1 KQAEQDKVAKASREAKKQVEKALEQKV 25
 Db 4 KQAEEDLIDASREAKKQQLDKVKQKVLE 28

RESULT 5
 US-08-302-756E-35
 ; Sequence 35, Application US/08302756E
 ; Patent No. 6737521
 GENERAL INFORMATION:
 APPLICANT: FISCHETTI, Vincent A.
 APPLICANT: POZZI, Gianni
 APPLICANT: SCHNEEWIND, Olaf
 TITLE OF INVENTION: DELIVERY AND EXPRESSION OF A HYBRID SURFACE PROTEIN ON THE SURFACE OF GRAM POSITIVE BACTERIA
 FILE REFERENCE: 016921-076
 CURRENT APPLICATION NUMBER: US/08/302,756E
 CURRENT FILING DATE: 1995-03-07
 PRIOR APPLICATION NUMBER: US 07/522,440
 PRIOR FILING DATE: 1990-05-11
 PRIOR APPLICATION NUMBER: US 07/742,199
 PRIOR FILING DATE: 1991-08-05
 PRIOR APPLICATION NUMBER: US 07/814,823
 PRIOR FILING DATE: 1991-12-23
 PRIOR APPLICATION NUMBER: US 07/851,082
 PRIOR FILING DATE: 1992-03-13
 PRIOR APPLICATION NUMBER: PCT/US93/02355
 PRIOR FILING DATE: 1993-03-12
 NUMBER OF SEQ ID NOS: 61
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 35
 LENGTH: 440
 TYPE: PRT
 ORGANISM: S. pyogenes
 US-08-302-756E-35

Query Match 52.6%: Score 72; DB 4; Length 440;
 Best Local Similarity 45.2%; Pred. No. 0.64%; Gaps 1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18;

Qy 5 DKVK-----ASREAKKQVEKALEQEDKV 28
 Db 270 DKYKEEKQISDASRQLRDLDSREAKKQVEKALEBANSKL 311

RESULT 6
 US-08-795-475-6
 ; Sequence 6, Application US/08795475
 ; Patent No. 5965390
 GENERAL INFORMATION:
 APPLICANT: Björck, Lars
 APPLICANT: Sjöbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 14

Query Match 52.6%: Score 72; DB 2; Length 443;
 Best Local Similarity 45.2%; Pred. No. 0.65%; Gaps 1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18;

Qy 5 DKVK-----ASREAKKQVEKALEQEDKV 28
 Db 272 DKYKEEKQISDASRQLRDLDSREAKKQVEKALEBANSKL 313

RESULT 7
 US-08-125-278B-6
 ; Sequence 6, Application US/08325278B
 ; Patent No. 6822075
 ; GENERAL INFORMATION:
 APPLICANT: Björck, Lars
 APPLICANT: Sjöbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed IP Law Group
 STREET: 701 Fifth Avenue Suite 6300
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278B
 FILING DATE: 26-Oct-1994
 CLASSIFICATION: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Potter, Jane E. R.
 REGISTRATION NUMBER: 33,332
 REFERENCE/DOCKET NUMBER: 100084-402
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 622-6031
 INFORMATION FOR SEQ ID NO: 6:

US-08-914-479A-4

Query Match 51.8%; Score 71; DB 4; Length 254;

Best Local Similarity 75.0%; Pred. No. 0.48; Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKKQVEKALEQLEDKV 28

Db 105 ASREAKKQVEKALEEANSKL 124

RESULT 11

US-08-914-479A-6

Sequence 6, Application US/08914479A

; Patent No. 6419932

GENERAL INFORMATION:

; APPLICANT: Dale, James B.

; TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER

; FILE REFERENCE: 81112.404C2

; CURRENT FILING DATE: 1997-08-19

; PRIOR APPLICATION NUMBER: 08/409,270

; PRIOR APPLICATION NUMBER: 1995-03-23

; PRIOR FILING DATE: 1992-09-16

; NUMBER OF SEQ ID NOS: 19

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 6

; LENGTH: 284

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier

; OTHER INFORMATION: of the COOH-terminal portion of M5

US-08-914-479A-6

Query Match 51.8%; Score 71; DB 4; Length 284;

Best Local Similarity 75.0%; Pred. No. 0.53; Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKKQVEKALEQLEDKV 28

Db 135 ASREAKKQVEKALEEANSKL 154

RESULT 12

US-08-917-271-10

Sequence 10, Application US/08937271

GENERAL INFORMATION:

; APPLICANT: Dale, James B.

; TITLE OF INVENTION: RECOMBINANT MULTIVALENT M PROTEIN

; NUMBER OF SEQUENCES: 40

; CORRESPONDENCE ADDRESS:

; ADDRESS: SEED and BERRY

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: 08/817-811

; FILING DATE: 14-APR-1997

; PRIORITY NUMBER: 08/817-811

; CLASSIFICATION: 424

; PRIORITY NUMBER: 08/817-811

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: WO 96/11944

; FILING DATE: 25-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: FBRC:005

; TELEPHONE: 512/418-3000

; INSTRUCTION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

NAME: Robbenman, Stephen J.

REGISTRATION NUMBER: 43,058

TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 632-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 305 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-917-271-10

Query Match 51.8%; Score 71; DB 3; Length 305;

Best Local Similarity 75.0%; Pred. No. 0.58; Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKKQVEKALEQLEDKV 28

Db 156 ASREAKKQVEKALEEANSKL 175

RESULT 13

US-08-817-811-66

Sequence 66, Application US/08817811

; Parent No. 6174528

GENERAL INFORMATION:

; APPLICANT: Cooper, Juan A.

; APPLICANT: Relf, Wendy A.

; APPLICANT: Good, Michael F.

; APPLICANT: Saul, Allan J.

; TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES

; TITLE OF INVENTION: COMPRISING SAME

; NUMBER OF SEQUENCES: 97

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/817,811

; FILING DATE: 14-APR-1997

; PRIORITY NUMBER: 08/817-811

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: WO 96/11944

; FILING DATE: 25-APR-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Highlander, Steven L.

; REGISTRATION NUMBER: 37,642

; REFERENCE/DOCKET NUMBER: FBRC:005

; TELEPHONE: 512/418-3000

; INSTRUCTION FOR SEQ ID NO: 66:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: linear

Query Match 50.0%; Score 68.5; DB 3; Length 28;

Best Local Similarity 55.2%; Pred. No. 0.096; Matches 16; Conservative 2; Mismatches 2; Indels 7; Gaps 1;

Qy 1 KQAEDKVKAASREAKKQVEKALEQLEDKVK 29
 Db 4 KQAEDRV-----QLEDRVEELQDKVK 25

RESULT 14
 US-08-817-811-52
 Sequence 52, Application US/08817811
 Patent No. 6174528
 GENERAL INFORMATION:
 APPLICANT: Cooper, Juan A.
 APPLICANT: Reli, Wendy A.
 APPLICANT: Good, Michael F.
 APPLICANT: Saul, Allan J.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 TITLE OF INVENTION: COMPRISING SAME
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Arnold, White & Durkee
 STREET: P.O. Box 4433
 CITY: Houston
 STATE: Texas
 ZIP: 77210
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/817,811
 FILING DATE: 14-APR-1997
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO 96/11944
 FILING DATE: 25-APR-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Highlander, Steven L.
 REGISTRATION NUMBER: 37,642
 REFERENCE/DOCKET NUMBER: FBRC:005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 512/418-3000
 TELEFAX: 512/474-7577
 INFORMATION FOR SEQ ID NO: 15:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-817-811-15

Query Match 47.8%; Score 65.5%; DB 3; Length 28;
 Best Local Similarity 58.6%; Pred. No. 0.21%;
 Matches 17; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

Qy 1 KQAEDKVKAASREAKKQVEKALEQLEDKVK 29
 Db 5 KQAERDLDASREAKK-----QLDKVK 26

Search completed: August 4, 2005, 08:38:31
 Job time : 40.4651 secs

US-08-817-811-52

SEQUENCE CHARACTERISTICS:
 LENGTH: 29 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear

Query Match 48.9%; Score 67; DB 3; Length 29;
 Best Local Similarity 48.3%; Pred. No. 0.15%;
 Matches 14; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

Qy 1 KQAEDKVKAASREAKKQVEKALEQLEDKVK 29
 Db 1 KQLEDKVMAQDTADRITLTKNQLEDKVK 29

RESULT 15
 US-08-817-811-15
 Sequence 15, Application US/08817811
 Patent No. 6174528
 GENERAL INFORMATION:
 APPLICANT: Cooper, Juan A.
 APPLICANT: Reli, Wendy A.
 APPLICANT: Good, Michael F.
 APPLICANT: Saul, Allan J.
 TITLE OF INVENTION: SYNTHETIC PEPTIDES AND VACCINES
 TITLE OF INVENTION: COMPRISING SAME
 NUMBER OF SEQUENCES: 97
 CORRESPONDENCE ADDRESS:

RESULT 2
 US-10-706-275-15
 ; Sequence 15, Application US/10706275
 ; Publication No. US2005000295611
 ; GENERAL INFORMATION:
 ; APPLICANT: ID Biomedical Corporation of Quebec
 ; APPLICANT: The Council of the Queensland Institute of Medical Research
 ; APPLICANT: Lowell, George H.
 ; APPLICANT: Burt, David S.
 ; APPLICANT: White, Gregory L.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Batzloff, Michael R.
 ; APPLICANT: Leandersson, Tomas B.
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: 021989-000710US
 ; CURRENT APPLICATION NUMBER: US/10/706,275
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIORITY APPLICATION NUMBER: US 60/426,409
 ; PRIORITY FILING DATE: 2002-11-15
 ; PRIORITY APPLICATION NUMBER: AU 2002302132
 ; PRIORITY FILING DATE: 2002-11-15
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 15
 ; LENGTH: 29
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE: Antigenic peptide sequence derivative of p145 base
 ; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
 ; US-10-706-275-15

Query Match 100.0%; Score 137; DB 17; Length 29;
 Best Local Similarity 100.0%; Pred. No. 7.8e-09;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 91.2%; Score 125; DB 17; Length 28;
 Best Local Similarity 92.9%; Pred. No. 1.7e-07;
 Matches 26; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match 1 KOAEQDKVAKSREAKKQVEKALEQLEDKV 28
 Qy 1 KOAEQDKVAKSREAKKQVEKALEQLEDKV 28
 Db 1 KOAEQDKVAKSREAKKQVEKALEQLEDKV 28

RESULT 4
 US-10-706-275-13
 ; Sequence 13, Application US/10706275
 ; Publication No. US2005000295611
 ; GENERAL INFORMATION:
 ; APPLICANT: ID Biomedical Corporation of Quebec
 ; APPLICANT: The Council of the Queensland Institute of Medical Research
 ; APPLICANT: Lowell, George H.
 ; APPLICANT: Burt, David S.
 ; APPLICANT: White, Gregory L.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Batzloff, Michael R.
 ; APPLICANT: Leandersson, Tomas B.
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: 021989-000710US
 ; CURRENT APPLICATION NUMBER: US/10/706,275
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIORITY APPLICATION NUMBER: US 60/426,409
 ; PRIORITY FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: AU 2002302132
 ; PRIOR FILING DATE: 2002-11-15
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 13
 ; LENGTH: 28
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
 ; US-10-706-275-13

Query Match 86.9%; Score 119; DB 17; Length 28;
 Best Local Similarity 89.3%; Pred. No. 8.3e-07;
 Matches 25; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Query Match 2 KOAEQDKVAKSREAKKQVEKALEQLEDKV 29
 Qy 2 KOAEQDKVAKSREAKKQVEKALEQLEDKV 29
 Db 1 KOAEQDKVAKSREAKKQVEKALEQLEDKV 29

RESULT 5
 US-10-706-275-14
 ; Sequence 14, Application US/10706275
 ; Publication No. US2005000295611
 ; GENERAL INFORMATION:
 ; APPLICANT: ID Biomedical Corporation of Quebec
 ; APPLICANT: The Council of the Queensland Institute of Medical Research
 ; APPLICANT: Lowell, George H.
 ; APPLICANT: Burt, David S.
 ; APPLICANT: White, Gregory L.
 ; APPLICANT: Good, Michael F.
 ; APPLICANT: Batzloff, Michael R.
 ; APPLICANT: Leandersson, Tomas B.
 ; TITLE OF INVENTION: Vaccine
 ; FILE REFERENCE: 021989-000710US
 ; CURRENT APPLICATION NUMBER: US/10/706,275
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIORITY APPLICATION NUMBER: US 60/426,409
 ; PRIORITY FILING DATE: 2002-11-15
 ; PRIOR APPLICATION NUMBER: AU 2002302132
 ; PRIOR FILING DATE: 2002-11-15
 ; NUMBER OF SEQ ID NOS: 15
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 12
 ; LENGTH: 28
 ; TYPE: PRT

PRIOR APPLICATION NUMBER: AU 2002302132
 PRIOR FILING DATE: 2002-11-15
 NUMBER OF SEQ ID NOS: 15
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 14
 LENGTH: 28
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
 US-10-706-275-14

Query Match Score 81.8%; Score 112; DB 17; Length 28;
 Best Local Similarity 88.9%; Pred. No. 5.2e-06;
 Matches 24; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 Software: PatentIn version 3.1
 SEQ ID NO: 10
 LENGTH: 28

Qy 3 AEDKVKA\$REAKKQVEKALEQLEDKVK 29
 Db 1 AEDKVQ\$REAKKQVEKALEQLEDKVQ 27

RESULT 6
 US-10-706-275-11
 / Sequence 11, Application US/10706275
 / Publication No. US200500029561
 / GENERAL INFORMATION
 / APPLICANT: ID Biomedical Corporation of Quebec
 / APPLICANT: The Council of the Queensland Institute of Medical Research
 / APPLICANT: Lowell, George H.
 / APPLICANT: Burt, David S.
 / APPLICANT: White, Gregory L.
 / APPLICANT: Good, Michael F.
 / APPLICANT: Batzloff, Michael R.
 / APPLICANT: Leanderison, Tomas B.
 / TITLE OF INVENTION: Vaccine
 / FILE REFERENCE: 021989-000710US
 / CURRENT APPLICATION NUMBER: US/10/706,275
 / CURRENT FILING DATE: 2003-11-13
 / PRIOR APPLICATION NUMBER: US 60/426,409
 / PRIOR FILING DATE: 2002-11-15
 / PRIOR APPLICATION NUMBER: AU 2002302132
 / PRIOR FILING DATE: 2002-11-15
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 11
 / LENGTH: 28
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
 US-10-706-275-11

Query Match Score 80.3%; Score 110; DB 17; Length 28;
 Best Local Similarity 85.2%; Pred. No. 8.7e-06;
 Matches 23; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Software: PatentIn version 3.1
 SEQ ID NO: 11
 LENGTH: 28

Qy 1 KQA\$BDKVKA\$REAKKQVEKALEQLEDK 27
 Db 2 KQA\$BDKVDA\$REAKKQVEKVKQLEDK 28

RESULT 7
 US-10-706-275-10
 / Sequence 10, Application US/10706275
 / Publication No. US200500029561
 / GENERAL INFORMATION
 / APPLICANT: ID Biomedical Corporation of Quebec
 / APPLICANT: The Council of the Queensland Institute of Medical Research
 / APPLICANT: Lowell, George H.
 / APPLICANT: Burt, David S.
 / APPLICANT: White, Gregory L.
 / APPLICANT: Good, Michael F.
 / APPLICANT: Batzloff, Michael R.
 / APPLICANT: Leanderison, Tomas B.
 / TITLE OF INVENTION: Vaccine
 / FILE REFERENCE: 021989-000710US
 / CURRENT APPLICATION NUMBER: US/10/706,275
 / CURRENT FILING DATE: 2003-11-13
 / PRIOR APPLICATION NUMBER: US 60/426,409
 / PRIOR FILING DATE: 2002-11-15
 / PRIOR APPLICATION NUMBER: AU 2002302132
 / PRIOR FILING DATE: 2002-11-15
 / NUMBER OF SEQ ID NOS: 15
 / SOFTWARE: PatentIn version 3.1
 / SEQ ID NO: 9
 / LENGTH: 28
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
 US-10-706-275-9

Query Match Score 59.1%; Score 81; DB 17; Length 28;
 Best Local Similarity 68.0%; Pred. No. 0.017;
 Matches 17; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
 Software: PatentIn version 3.1
 SEQ ID NO: 9
 LENGTH: 28

Qy 1 KQA\$BDKVKA\$REAKKQVEKALEQLEDK 25
 Db 4 KQA\$DD\$DASREAKKQVKVQLEDK 28

RESULT 9
 US-08-325-278-6
 / Sequence 6, Application US/08325278
 / Publication No. US20030027283A1
 / GENERAL INFORMATION
 / APPLICANT: The Council of the Queensland Institute of Medical Research
 / APPLICANT: Lowell, George H.
 / APPLICANT: Burt, David S.
 / APPLICANT: White, Gregory L.
 / APPLICANT: Good, Michael F.
 / APPLICANT: Batzloff, Michael R.

APPLICANT: Björck, Lars
 APPLICANT: Sjöbring, Ulf
 TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SEED and BERRY LLP
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: USA
 ZIP: 98104-7092
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/325,278
 FILING DATE: 26-OCT-1996
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: McMasters, David D.
 REGISTRATION NUMBER: 33,963
 REGISTRATION/DOCKET NUMBER: 450023-401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 622-4900
 TELEFAX: (206) 682-6031
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 443 amino acids
 TYPE: amino acid
 MOLECULE TYPE: protein
 MOLECULE TYPE: linear
 US-08-325-278-6

Query Match Score 52.6%; Length 443;
 Best Local Similarity 45.2%; Pred. No. 3.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Qy 5 DKVK-----ASREAKQVEKALBQLEDKV 28
 Db 272 DKVKEEKQISDASRQRURLDASREAKQVEKALEANSKL 313

RESULT 10
 US-10-474-792-672
 / Sequence 672, Application US/10474792
 / Publication No. US20040236072A1
 / GENERAL INFORMATION:
 / APPLICANT: Olmsted, Stephen
 / APPLICANT: Zagursky, Robert
 / APPLICANT: Nickbarg, Elliot
 / APPLICANT: Winter, Lourie
 / TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
 / FILE REFERENCE: AM 100399
 / CURRENT APPLICATION NUMBER: US/10/474,792
 / CURRENT FILING DATE: 2003-10-14
 / NUMBER OF SEQ ID NOS: 674
 / SEQ ID NO: 672
 / LENGTH: 553
 / TYPE: PRT
 / ORGANISM: Streptococcus Pyogenes
 US-10-474-792-672

Query Match Score 52.6%; Length 553;
 Best Local Similarity 45.2%; Pred. No. 4.3;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Qy 5 DKVK-----ASREAKQVEKALBQLEDKV 28
 Db 382 DKVKEEKQISDASRQRURLDASREAKQVEKALEANSKL 423

RESULT 11
 US-10-732-923-3295
 / Sequence 3295, Application US/10732923
 / Publication No. US20050108791A1
 / GENERAL INFORMATION:
 / APPLICANT: Edgeton, Michael D
 / TITLE OF INVENTION: TRANSENSENIC PLANTS WITH IMPROVED PHENOTYPES
 / FILE REFERENCE: 38-15(52786)C
 / CURRENT APPLICATION NUMBER: US/10/732,923
 / CURRENT FILING DATE: 2003-12-10
 / PRIOR APPLICATION NUMBER: 10/310,154
 / PRIOR FILING DATE: 2002-11-04
 / NUMBER OF SEQ ID NOS: 24149
 / SEQ ID NO: 3295
 / LENGTH: 558
 / TYPE: PRT
 / ORGANISM: Streptococcus Pyogenes
 US-10-732-923-3295

Query Match Score 52.6%; Length 558;
 Best Local Similarity 50.0%; Pred. No. 4.3;
 Matches 18; Conservative 3; Mismatches 7; Indels 8; Gaps 1;

Qy 1 KQAED-----KTRASREAKQVEKALBQLEDKV 28
 Db 393 KQTSDASRQGLRRDLDASREAKQVEKALEANSKL 428

RESULT 12
 US-10-141-627-4
 / Sequence 4, Application US/10141627
 / Publication No. US2002017663A1
 / GENERAL INFORMATION:
 / APPLICANT: Dale, James B.
 / TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
 / FILE REFERENCE: 481112-404C3
 / CURRENT APPLICATION NUMBER: US/10/141,627
 / CURRENT FILING DATE: 2005-05-07
 / NUMBER OF SEQ ID NOS: 19
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO: 4
 / LENGTH: 254
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: An antigen of M5 and a carrier of the
 / COOH-terminal portion of M5
 US-10-141-627-4

Query Match Score 51.8%; Length 254;
 Best Local Similarity 75.0%; Pred. No. 2.4;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKQVEKALBQLEDKV 28
 Db 105 ASREAKQVEKALBANSKL 124

RESULT 13
 US-10-141-627-6
 / Sequence 6, Application US/10141627
 / Publication No. US2002017663A1
 / GENERAL INFORMATION:
 / APPLICANT: Dale, James B.
 / TITLE OF INVENTION: ANTIGEN OF HYBRID M PROTEIN AND CARRIER
 / FILE REFERENCE: 481112-404C3
 / CURRENT APPLICATION NUMBER: US/10/141,627
 / CURRENT FILING DATE: 2002-05-07
 / NUMBER OF SEQ ID NOS: 19
 / SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 6
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: An antigen of three fragments of M5 and a carrier
; OTHER INFORMATION: Of the COOH-terminal portion of M5
US-10-141-627-6

Qy      9 ASBREAKKQVEKALEQLEDKV 28
Db      135 ASBREAKKQVEKALEEANSKL 154

RESULT 14
US-10-282-122A-67145
; Sequence 67145, Application US/10282122A
; PUBLICATION No. US20040029129A1
; GENERAL INFORMATION
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.

; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: EIJTRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 67145
; LENGTH: 389
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-10-282-122A-67145

Query Match      48.9% Score 67; DB 15; Length 389;
; Best Local Similarity 51.6%; Pred. No. 11;
; Matches 16; Conservative 5; Mismatches 8; Indels 2; Gaps 1;

Db      175 KOABEEAKAKAABEKKAKAKAAEAKAK 205

RESULT 15
US-10-706-275-8
; Sequence 8, Application US/10706275
; Publication No. US20050002956A1
; GENERAL INFORMATION
; APPLICANT: ID Biomedical Corporation of Quebec
; APPLICANT: The Council of the Queensland Institute of Medical Research
; APPLICANT: Lowell, George H.
; APPLICANT: Burt, David S.
; APPLICANT: White, Gregory L.
; APPLICANT: Good, Michael F.
; APPLICANT: Battloff, Michael R.
; APPLICANT: Leanderson, Tomas B.
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: 021989-000710US
; CURRENT APPLICATION NUMBER: US/10/706,275
; CURRENT FILING DATE: 2003-11-13
; PRIOR APPLICATION NUMBER: US 60/426,409
; PRIOR FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: AU 2002302132
; PRIOR FILING DATE: 2002-11-15
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 8
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: antigenic peptide sequence derivative of p145 base
US-10-706-275-8

Query Match      47.8% Score 65.5; DB 17; Length 28;
; Best Local Similarity 58.6%; Pred. No. 0.99;
; Matches 17; Conservative 2; Mismatches 3; Indels 7; Gaps 1;

Qy      1 KOAEDKYKASREAKKQVEKALEQLEDKV 29
Db      5 KOAERDIDASREAKK-----QLQDKVK 26

Search completed: August 4, 2005, 08:55:14
Job time: 142.628 sec

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GenCore version 5.1.6
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OM protein - protein search, using sw model
 Run on: August 4, 2005, 08:50:19 ; Search time 31.6977 Seconds
 (without alignments)
 88.028 Million cell updates/sec

Title: US-10-706-275-2
 Perfect score: 137
 Sequence: 1 KQAEKVKASREAKKVKEAKALEQEDRVK 29

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
 Maximum DB seq length: 20000000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing First 45 summaries

Database : PIR 79:
 1: pir1:
 2: pir2:
 3: pir3:
 4: pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	72.5	52.9	587	JC1419	PC gamma (IgG) rec
2	72	52.6	388	A49545	plasminogen-binding protein M precursor
3	72	52.6	408	S30283	M protein precursor
4	72	52.6	436	S30284	plasminogen-binding protein
5	72	52.6	454	S43556	M protein precursor
6	72	52.6	472	S43554	plasminogen-binding protein
7	72	52.6	483	A26297	M6 protein - Strep
8	72	52.6	484	S31401	M1 protein precursor
9	72	52.6	484	S44489	M1 protein precursor
10	72	52.6	484	S34978	M1 protein precursor
11	72	52.6	501	A44643	M protein precursor
12	72	52.6	532	S54871	M protein - Strep
13	72	52.6	564	A60115	M protein precursor
14	71	51.8	492	A28516	M5 protein precurs
15	71	51.8	539	A28549	M24 protein precurs
16	70	51.1	528	S57835	IgG-binding protein
17	66	48.2	1365	T45031	hypothetical prote
18	66	48.2	1408	T45039	hypothetical prote
19	64	46.7	217	G15219	hypothetical prote
20	63.5	46.4	104	I1	conserved hypothet
21	62	45.3	493	T22180	hypothetical prote
22	61	44.5	445	T50972	probable zutoin [i
23	60	43.8	284	S22470	beta-tropomyosin -
24	60	43.8	876	A0843	alanine tRNA ligas
25	59	43.1	284	TMRKF	tropomyosin beta C
26	59	43.1	284	F1	tropomyosin 1, emb
27	59	43.1	284	A25562	tropomyosin 1, fib
28	59	43.1	284	S0922	tropomyosin beta,
29	59	43.1	284	A44131	tropomyosin beta 2

ALIGNMENTS

RESULT 1
 JC1419
 FC Gamma (IgG) receptor II precursor - Streptococcus sp.
 N;Alternate names: Fcrv protein
 C;Species: Streptococcus sp.
 C;Date: 30-Sep-1993 #sequence revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: JC1419; S17354
 R;Smirnov, O.Y.; Dembsuk, A.I.; Zakharov, M.V.; Abramov, V.M.; Zav'yalov, V.P.
 Gene 120, 27-32, 1992
 A;Title: Protein V, a novel type-II IgG receptor from Streptococcus sp. : Sequence, homologous
 A;Reference number: JC1419; MUID:93013016; PMID:1398120
 A;Accession: JC1419
 A;Molecule type: DNA
 A;Residues: 1-587 <SMI>
 A;Cross-references: UNIPROT:Q55312; EMBL:X62467; NID:947562; PIDN:CAA44324.1; PID:947556
 A;Experimental source: strain 22/58'Valente'
 C;Genetics:
 A;Gene: fcrv
 C;Superfamily: M5 protein
 C;Keywords: duplication; immunoglobulin receptor
 F;1-41/Domain: signal sequence #status Predicted <SIG>
 F;42-87/Product: IgG Fc receptor II #status Predicted <MAT>
 F;234-268/Region: 35-residue repeat A
 F;269-303/Region: 35-residue repeat A
 F;304-338/Region: 35-residue repeat A
 F;339-373/Region: 35-residue repeat A
 F;374-408/Region: 35-residue repeat B
 F;416-450/Region: 35-residue repeat B

Query Match 52.9%; Score 72.5%; DB 2; Length 587;
 Best Local Similarity 46.3%; Pred. No. 2.5;
 Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;

Qy 1 KQAEDK-----VKAERKQVKVKALEQEDKV 28
 Db 417 KVKEDKQISDASRQRGLDRDLSRAEKVKQVKVKALEEANSKL 457

RESULT 2
 A49545
 Plasminogen-binding protein PAM precursor - Streptococcus pyogenes (fragment)
 N;Alternate names: plasminogen-binding M-like protein (Pd 53)
 C;Species: Streptococcus pyogenes
 C;Date: 23-Mar-1995 #sequence revision 05-Apr-1995 #text_change 09-Jul-2004
 C;Accession: A49545; S61084; S60829; S70459; S32619
 R;Berge, A.; Sjoerbring, U.
 J. Biol. Chem., 268, 25417-25424, 1993
 A;Title: PAM, a novel plasminogen-binding protein from Streptococcus pyogenes.
 A;Reference number: A49545; MUID:94064605; PMID:8244975
 A;Accession: A49545
 A;Molecule type: DNA
 A;Residues: 1-388 <BBR>

A;Cross-references: UNIPROT:P49054; EMBL:Z22219; NID:g288978; PIDN:CAA80222.1; PID:99408
 R;Whatmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
 Submitted to the EMBL Data Library, July 1994
 A;Description: Noncongruent relationships between variation in emm1 gene sequences and t
 A;Accession: S61072
 A;Molecule type: DNA
 A;Residues: 13-96 <WHA>
 A;Cross-references: EMBL:U11975; NID:g533627; PIDN:AAA9591.1; PID:g1235829
 A;Experimental source: serotype M53
 R;Whatmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
 Mol. Microbiol. 14, 619-631, 1994
 A;Title: Non-congruent relationships between variation in emm gene sequences and the pop
 A;Accession number: S60784; MUID:95198537; PMID:791551
 A;Accession: S60829
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 17-77 <WHA>
 A;Cross-references: EMBL:U11975
 A;Experimental source: serotype M53
 R;Carlsson Wistedt, A.; Ringdahl, U.; Mueller-Esterl, W.; Sjoerbring, U.
 Mol. Microbiol. 18, 569-578, 1995
 A;Title: Identification of a plasminogen-binding motif in PAM, a bacterial surface prote
 A;Reference number: S70457; MUID:96342365; PMID:8748039
 A;Accession: S70459
 A;Molecule type: DNA
 A;Residues: 30-162 <CAR>
 C;Superfamily: M5 protein
 C;Keywords: cell wall
 F;1-29/Domain: signal sequence (fragment) #status predicted <SIG>
 F;30-388/Product: plasminogen-binding protein PAM #status predicted <MAT>
 Query Match 52 6%; Score 72; DB 2; Length 388;
 Best Local Similarity 45.2%; Pred. No. 1.9;
 Matches 19; Conservative 2; Mismatches 3; Indels 1;
 Gaps 1;
 Qy 5 DVKV-----ASRAEKQVEKALEQLEDKV 28
 Db 244 DVKVKEEKQISDASRQGLRRDLDASRAEKQVEKALEBEANSKL 285

RESULT 3
 S3023
 C;Species: Streptococcus pyogenes (serotype M41)
 C;Accession: S30283; S29680
 R;Podbielski, A.
 Mol. Gen. Genet. 237, 287-300, 1993
 A;Title: Three different types of organization of the vir regulon in group A streptococco
 A;Accession number: S30283; MUID:93204905; PMID:8455563
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-408 <POD1>
 A;Cross-references: UNIPROT:Q54837; EMBL:X58178
 R;Podbielski, A.; Melzer, B.
 Submitted to the EMBL Data Library, February 1991
 A;Description: Pcr mediated cloning and sequencing of group A streptococcal emm41/52 (ev
 A;Accession: S29680
 A;Molecule type: DNA
 A;Residues: 1-230, 'N'-232-371, 'R', 373-408 <POD2>
 A;Cross-references: EMBL:X58178; NID:g47362; PIDN:CAA41167.1; PID:g47363
 C;Genetics:
 A;Gene: emm
 C;Superfamily: M5 protein
 C;Keywords: transmembrane protein
 F;1-408/Product: M protein #status predicted <SIG>
 F;42-408/Product: M protein #status predicted <MAT>
 F;383-401/Domain: transmembrane #status predicted <MM>

Query Match 52.6%; Score 72; DB 2; Length 436;
 Best Local Similarity 45.2%; Pred. No. 2.1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18;
 Gaps 1;
 Qy 5 DVVK-----ASRAEKQVEKALEQLEDKV 28
 Db 265 DVKVKEEKQISDASRQGLRRDLDASRAEKQVEKALEBEANSKL 306

RESULT 4
 S30284
 C;Species: Streptococcus pyogenes (serotype M52)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
 C;Accession: S30284; S29681
 R;Podbielski, A.
 Mol. Gen. Genet. 237, 287-300, 1993
 A;Title: Three different types of organization of the vir regulon in group A streptococc
 A;Reference number: S30283; MUID:93204905; PMID:8455563
 A;Status: nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-436 <POD1>
 A;Cross-references: UNIPROT:Q54839; EMBL:X58179
 R;Podbielski, A.; Melzer, B.
 Submitted to the EMBL Data Library, February 1991
 A;Description: Pcr mediated cloning and sequencing of group A streptococcal emm41/52 (ev
 A;Accession number: S29680
 A;Molecule type: DNA
 A;Cross-references: EMBL:X58179; NID:g47364; PIDN:CAA41168.1; PID:g47365
 C;Genetics:
 A;Gene: emm
 C;Superfamily: M5 protein
 C;Keywords: transmembrane protein
 F;1-41/Domain: signal sequence #status predicted <SIG>
 F;42-436/Product: M protein #status predicted <MT>
 F;411-429/Domain: transmembrane #status predicted <MM>
 Query Match 52.6%; Score 72; DB 2; Length 436;
 Best Local Similarity 45.2%; Pred. No. 2.1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18;
 Gaps 1;

Query Match 52 6%; Score 72; DB 2; Length 436;
 Best Local Similarity 45.2%; Pred. No. 2.1;
 Matches 19; Conservative 2; Mismatches 3; Indels 18;
 Gaps 1;
 Qy 5 DVVK-----ASRAEKQVEKALEQLEDKV 28
 Db 310 DVKVKEEKQISDASRQGLRRDLDASRAEKQVEKALEBEANSKL 351

RESULT 6
 S43554 plasminogen-binding protein MLG72 - Streptococcus sp. (fragment)
 C;Species: Streptococcus sp.
 A;Variety: group G
 C;Date: 07-Sep-1994 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000
 C;Accession: S43599; S43554
 R;ben Nasr, A.; Wistedt, A.; Ringdahl, U.; Sjoesbring, U.
 Eur. J. Biochem. 222, 267-276, 1994
 A;Title: Streptokinase activates plasminogen bound to human group C and G streptococci
 A;Reference number: S43598; MUID:94291620; PMID:8020466
 A;Accession: S43599
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-472 <B62>
 A;Cross-references: EMBL:232678; NID:9474769; PIDN:CAA83589.1; PID:91333838
 C;Superfamily: M5 protein

Query Match 52.6%; Score 72; DB 2; Length 472;
 Best Local Similarity 45.2%; Pred. No. 2.3;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
 Qy 5 DKVK-----ASREAKQVEKALEQLEDKV 28
 Db 328 DKVKEEKQISDTSRKGLRDLDAASREAKQVEKALEBANSKL 369

RESULT 7
 A26297 M6 protein - Streptococcus pyogenes

C;Species: Streptococcus pyogenes
 C;Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
 C;Accession: A26297
 R;Hollingshead, S.K.; Fischetti, V.A.; Scott, J.R.
 J. Biol. Chem. 261, 1677-1686, 1986
 A;Title: Complete nucleotide sequence of type 6 M protein of the group A streptococcus.
 A;Reference number: A26297; MUID:86111835; PMID:3511046
 A;Accession: A26297
 A;Molecule type: DNA
 A;Residues: 1-483 <HOL>
 A;Cross-references: UNIPROT:P08089; GB:M11338; GB:M11415; NID:9153699; PIDN:AAA26920.1;
 C;Keywords: coiled coil; transmembrane protein
 C;Genetics:

Query Match 52.6%; Score 72; DB 2; Length 483;
 Best Local Similarity 45.2%; Pred. No. 2.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
 Qy 5 DKVK-----ASREAKQVEKALEQLEDKV 28
 Db 312 DKVKEEKQISDTSRKGLRDLDAASREAKQVEKALEBANSKL 353

RESULT 8
 S35401 M1 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: S35401; S61074; S60784
 R;Pabiecki, A.
 Submitted to the EMBL Data Library, September 1991
 A;Reference number: S35401
 A;Accession: S35401
 A;Molecule type: DNA
 A;Residues: 1-484 <PDB>
 A;Cross-references: UNIPROT:Q10372; EMBL:X62131; NID:9111757; PID:CAA44062.1; PID:931177
 R;Whitmore, A.; Kapur, V.; Sullivan, D.; Musser, J.; Kehoe, M.
 Submitted to the EMBL Data Library, July 1994
 A;Description: Noncongruent relationships between variation in emm1 gene sequences and

A;Reference number: S61072
 A;Accession: S61074
 A;Molecule type: DNA
 A;Residues: 16-54 <WHA>
 A;Cross-references: EMBL:U11940; NID:9533557; PIDN:AAA99556.1; PID:9533558
 R;Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.

Mol. Microbiol. 14, 619-631, 1994
 A;Title: Non-congruent relationships between variation in emm gene sequences and the protein
 A;Reference number: S60784; MUID:95198537; PMID:7891551
 A;Accession: S60784
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 29-89 <WHA>
 A;Cross-references: EMBL:U11940
 C;Genetics:
 C;Superfamily: M5 protein

Query Match 52.6%; Score 72; DB 2; Length 484;
 Best Local Similarity 45.2%; Pred. No. 2.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
 Qy 5 DKVK-----ASREAKQVEKALEQLEDKV 28
 Db 313 DKVKEEKQISDTSRKGLRDLDAASREAKQVEKALEBANSKL 354

RESULT 9
 S46489 M1 protein precursor - Streptococcus pyogenes

C;Species: Streptococcus pyogenes
 C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C;Accession: S46489; S46490
 R;Akesson, P.; Schmidt, K.H.; Cooney, J.; Bjoerck, L.
 Biochem. J. 300, 877-886, 1994
 A;Title: M1 protein and protein H: IgGFC- and albumin-binding streptococcal surface proteins
 A;Reference number: S46489; MUID:94280417; PMID:8010973
 A;Accession: S46489
 A;Molecule type: DNA
 A;Residues: 1-484 <AKB>
 A;Cross-references: UNIPROT:Q05464; UNIPROT:Q10372; UNIPROT:Q99XV0
 A;Experimental source: strain 40/58, serotype M1
 A;Accession: S46490
 A;Molecule type: protein
 A;Residues: 42-51 <AKW>
 A;Experimental source: strain 40/58, serotype M1
 C;Genetics:
 A;Gene: emm1
 C;Superfamily: M5 protein
 C;Keywords: transmembrane protein

F;1-41/Domain: signal sequence #status predicted <SIG>
 P;42-484/Product: M1 protein #status experimental <MAT>
 P;459-477/Domain: transmembrane #status predicted <TMM>
 Query Match 52.6%; Score 72; DB 2; Length 484;
 Best Local Similarity 45.2%; Pred. No. 2.4;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;
 Qy 5 DKVK-----ASREAKQVEKALEQLEDKV 28
 Db 313 DKVKEEKQISDTSRKGLRDLDAASREAKQVEKALEBANSKL 354

RESULT 10
 S34978 M1.1 protein precursor - Streptococcus pyogenes
 C;Species: Streptococcus pyogenes
 C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C;Accession: S34978; S31166
 R;Harbaugh, M.P.; Podbielski, A.; Huegli, S.; Cleary, P.P.
 Mol. Microbiol. 8, 981-991, 1993
 A;Title: Nucleotide substitutions and small-scale insertion produce size and antigenic variations

Search completed: August 4, 2005, 09:04:11
 Job time : 32.6977 secs

RESULT 14

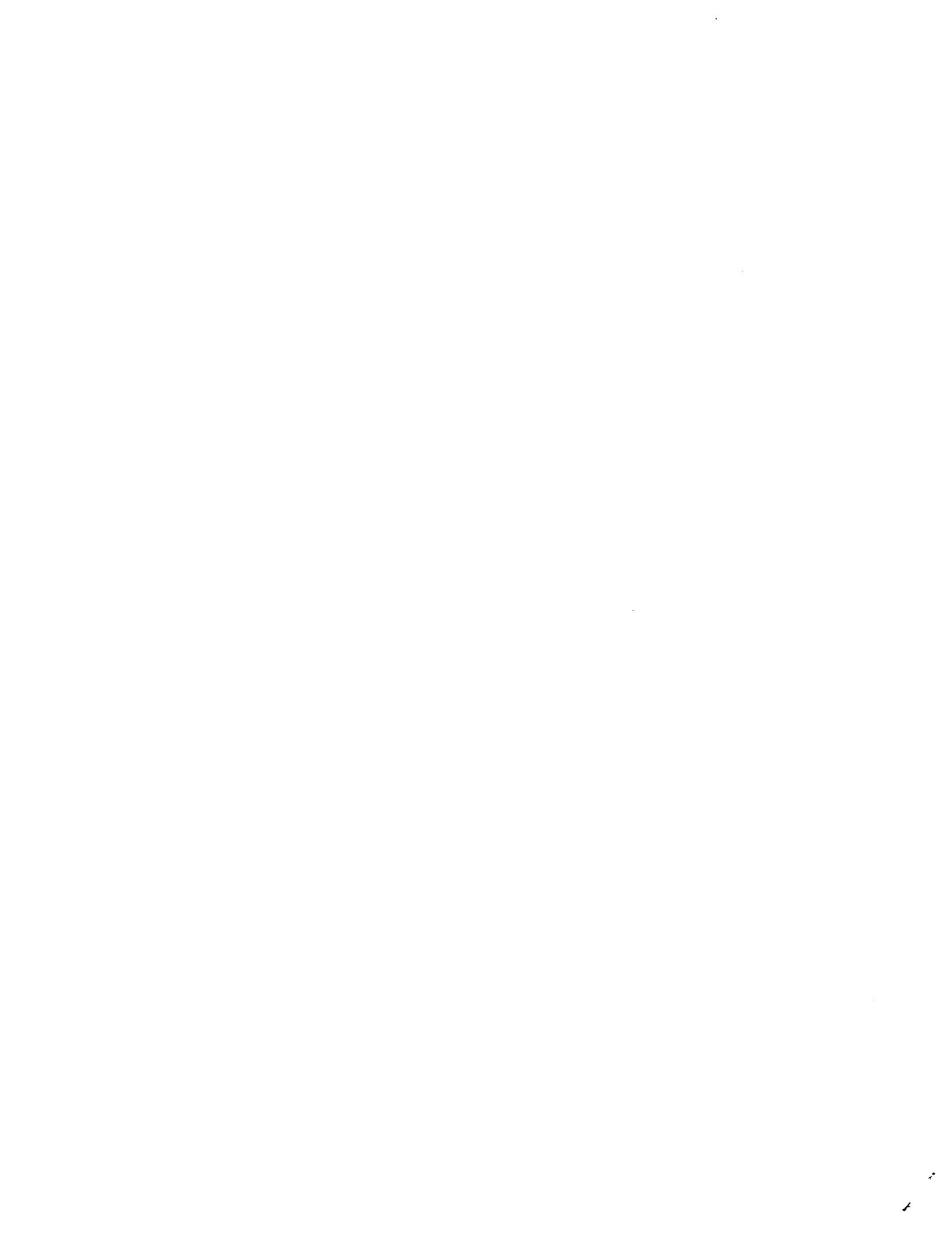
Qy 5 DKVK-----ASREAKQVEKALEQLEDKV 28
 C:Species: Streptococcus pyogenes
 C:Variety: serotype M5
 C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 09-Jul-2004
 C:Accession: A28616; S60787
 A:Title: Antigenic variation among group A streptococcal M proteins. Nucleotide sequence
 A:Reference number: A28616; MUID:80186881; PMID:3281944
 A:Accession: A28616
 A:Molecule type: DNA
 A:Residues: 1-492 <WHA>
 A:Cross-references: UNIPROT:P02977; GB:M20374; PID:9153812; PID:9153813
 R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
 Mol. Microbiol. 14, 619-631, 1994
 A:Title: Non-congruent relationships between variation in emm gene sequences and the pop
 A:Reference number: S60784; MUID:95198537; PMID:7891551
 A>Status: Preliminary: nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: DNA
 A:Residues: 30-89 <WHA>
 C:Genetics:
 C:Gene: smp5
 C:Superfamily: M5 protein
 C:Keywords: coiled coil; transmembrane protein
 C:Domain: Signal sequence #status Predicted <SIG>
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Query Match 51.8%; Score 71; DB 2; Length 492;
 Best Local Similarity 75.0%; Fred. No. 3;
 Matches 15; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 9 ASREAKQVEKALEQLEDKV 28
 C:Species: Streptococcus pyogenes
 C:Variety: serotype M24
 C:Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 09-Jul-2004
 C:Accession: A28549; S60042
 A:Title: Molecular evolution of streptococcal M protein: cloning and nucleotide sequence
 A:Reference number: A28549; MUID:88115166; PMID:3276665
 A:Accession: A28549
 A:Molecule type: DNA
 A:Residues: 1-539 <MOU>
 A:Cross-references: UNIPROT:PI2379; GB:M19031; PID:9153616; PID:9153674; 1, PID:9153617
 R:Whitmore, A.M.; Kapur, V.; Sullivan, D.J.; Musser, J.M.; Kehoe, M.A.
 Mol. Microbiol. 14, 619-631, 1994
 A:Title: Non-congruent relationships between variation in emm gene sequences and the pop
 A:Reference number: S60784; MUID:95198537; PMID:7891551
 A>Status: Preliminary: nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: DNA
 A:Residues: 30-89 <WHA>
 C:Superfamily: M5 protein
 C:Keywords: coiled coil; transmembrane protein

Query Match 51.8%; Score 71; DB 2; Length 539;

Best Local Similarity 75.0%; Fred. No. 3;



Scoring table:	BLOSUM62	ALIGNMENTS			
Searched:	1612378 seqs, 512079187 residues				
Total number of hits satisfying chosen parameters:	1612378				
Minimum DB seq length:	0				
Maximum DB seq length:	2000000000				
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries				
Database :	UniProt_03: 1: uniprot_sprot: 2: uniprot_trembl: *				
Pred.	No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.				
SUMMARIES					
Result No.	Query Match	Description			
Score	Length	ID			
Match	DB				
1	74.5	54.4	592	2	Q00720
2	72.5	52.9	454	2	Q84077
3	72.5	52.9	550	2	Q54840
4	72.5	52.9	587	2	Q55312
5	72	52.6	100	2	Q54639
6	72	52.6	100	2	Q54640
7	72	52.6	100	2	Q9R3A1
8	72	52.6	198	2	Q54832
9	72	52.6	208	2	P95824
10	72	52.6	208	2	P95826
11	72	52.6	237	2	Q6TLR5
12	72	52.6	251	2	Q8V9Q3
13	72	52.6	279	2	Q8GLB7
14	72	52.6	282	2	Q8GLA6
15	72	52.6	303	2	Q8GL98
16	72	52.6	307	2	Q8GL84
17	72	52.6	314	2	Q8GLB0
18	72	52.6	317	2	Q8GL92
19	72	52.6	319	2	Q8GLA2
20	72	52.6	322	2	Q8GLA4
21	72	52.6	326	2	Q8GL91
22	72	52.6	340	2	Q8GLA1
23	72	52.6	369	2	Q8GL90
24	72	52.6	388	1	PAM_STRPY
25	72	52.6	400	2	Q8NZ79
26	72	52.6	408	2	Q54837
27	72	52.6	435	2	Q8AMM3
28	72	52.6	436	2	Q54839
29	72	52.6	441	2	Q55246
30	72	52.6	443	2	Q54703
31	72	52.6	454	2	Q55278
32	72	52.6	465	2	Q83XW0
33	72	52.6	483	1	Q55279
34	72	52.6	484	2	Q05464
35	72	52.6	484	2	Q10372
36	72	52.6	484	2	Q99XV0
37	72	52.6	488	2	Q54830
38	72	52.6	488	2	Q9rhv2
39	72	52.6	508	2	Q76mJ2
40	72	52.6	532	2	Q55098
41	72	52.6	558	2	Q54718
42	72	52.6	564	1	M12_STRPY
43	72	52.6	581	2	Q54635
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45	72	52.6	581	2	Q8K5P9
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Perfect score:	137				
Sequence:	1 KQADKVKAASREAKVKQVEKALEQLEDKVK 29				
Copyright (c) 1993 - 2005 Compugen Ltd.					
OM protein - protein search, using sw model					
Run on:	August 4, 2005, 08:38:38 ; Search time 153.767 Seconds 96.576 Million cell updates/sec				
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SEARCHED					
RESULT 1					
Q00720	PRELIMINARY;	PRT; 592 AA.			
ID Q00720;					
AC Q00720;					
DT 01-NOV-1996 ("TREMBLrel. 01, Created)					
DT 01-NOV-1996 ("TREMBLrel. 01, Last sequence update)					
DT 01-MAR-2004 ("TREMBLrel. 26, Last annotation update)					
DB M protein precursor.					
OS Streptococcus sp. (Lancefield group G).					
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;					
CC NCBI_TaxID=1320;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=1750;					
RX MEDLINE=92363566; PubMed=1500178;					
RA Collins C.M., Kimura A., Biino A.L.;					
RT "Group G streptococcal M protein exhibits structural features analogous to class I M proteins of group A streptococci.";					
RL Infect. Immun. 60:3689-3696 (1992).					
CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).					
DR EMBL: M9574; AAA2628.1;					
DR GO: 0009986; C:cell surface; I:EA.					
DR GO: 0005618; C:cell wall; I:EA.					
DR GO: 0016020; C:membrane; I:EA.					
DR InterPro: IPR011000; Apolp_III like.					
DR InterPro: IPR005877; Gps_YSIRK.					
DR InterPro: IPR001899; Gram_pos_anchor.					
DR InterPro: IPR003345; M_repeat_-.					
DR Pfam: PF00746; Gram_Pos_anchor; 1.					
DR Pfam: PF03370; M; 2.					
DR Pfam: PF00650; YSIRK signal; 1.					
DR PRINTS: PRO0015; GPO_SANCHOR.					
DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.					
DR TIGRFAMs; TIGR01168; YSIRK_signal; 1.					
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.					
KW Cell wall; Peptidoglycan-anchor; Signal; 1.					
FT SIGNAL 1 41		Potential.			
FT CHAIN 1 41		M protein.			
SQ SEQUENCE 592 AA; 67008 MW; 821399D030DE5CEB CRC64;					
Query Match 54.4%; Score 74.5%; DB 2; Length 592;					
Best Local Similarity 46.3%; Pred. No. 16;					
Matches 19; Conservative 4; Mismatches 5; Indels 13; Gaps 1;					
Qy 1 KQADKVKAASREAKVKQVEKALEQLEDKV 28					
Db 422 KVKEDKQISDASRKGLRRDLEASRAKKQVEKALEEANSKL 462					
RESULT 2					
Q840T7	PRELIMINARY;	PRT; 454 AA.			
ID Q840T7					

AC	QB4OT7;	DT 01-JUN-2003 (TREMBLrel. 24, Created)	Qy 1 KQAEDK-----VKASREAKKQVEKALEQLEDKV 28	Db 381 KVKEDKQISDASRKGRLRDASREAKKQVEKALEBANSKL 421
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	M protein (Fragment).			
OS	Streptococcus pyogenes.			
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.			
NCBI_TaxID=1314;				
RN [1]	SEQUENCE FROM N.A. Sripakash K.S.; Dyal-Smith M.L. to the EMBL/GenBank/DDJB databases.			
RA	Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.			
RL	EMBL; AY263878; A4092603; 1;			
DR	GO: 0016020; C membrane; IEA.			
DR	InterPro: IPR003345; M_repeat.			
Pfam; PF02370; M; 1.				
FT NON_TER 1 1				
FT NON_TER 454 454				
SEQID 454 AA; 51368 MW; 4DF100DA6467864 CRC64;				
Query Match Score 52.9%; Pred. No. 20; Length 454;				
Best Local Similarity 46.3%; Mismatches 3; Indels 13; Gaps 1;				
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;				
Qy 1 KQAEDK-----VKASREAKKQVEKALEQLEDKV 28				
Db 381 KVKEDKQISDASRKGRLRDASREAKKQVEKALEBANSKL 421				
RESULT 3				
Q54840	PRELIMINARY;	PRT; 550 AA.		
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AC	O54840;	Created)		
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DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	M protein.			
GN	Name=emm55;			
OS	Streptococcus pyogenes.			
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;				
OC	Streptococcus.			
NCBI_TaxID=1314;				
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Query Match Score 52.9%; Pred. No. 20; Length 454;				
Best Local Similarity 46.3%; Mismatches 3; Indels 13; Gaps 1;				
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;				
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Db 381 KVKEDKQISDASRKGRLRDASREAKKQVEKALEBANSKL 421				
RESULT 4				
Q55312	PRELIMINARY;	PRT; 587 AA.		
ID Q55312;				
AC	Q55312;	Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)			
DB	Protein V precursor.			
GN	Name=fcrv;			
OS	Streptococcus sp.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
Strptococcus.				
NCBI_TaxID=1306;				
OX [1]; RN				
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Valente;			
RX	MEDLINE=93013016; PubMed=13981120; DOI=10.1016/0378-1119(92)90005-A;			
RA	Denesuk O.Y., Denesuk A.I., Zakharov M.V., Abramov V.M.,			
RA	Zav'yalov V.P.;			
RT	"Protein V, a novel type-II IgG receptor from Streptococcus sp.:			
RT	sequence, homologies and putative IgG-binding site."			
RL	Gene 120:27-32 (1992).			
CC	- - SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).			
CC	EMBL; XG2467; CAA44324.1; -.			
DR	PIR; JCI419; JCI419.			
DR	HSSP; Q15813; ID2M.			
DR	GO; GO:0005618; C-cell surface; IEA.			
DR	GO; GO:001020; C-cell wall; IEA.			
DR	InterPro; IPR005877; Grammembrane; IEA.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	InterPro; IPR003345; M_repeat.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF02370; M; 1.			
DR	Pfam; PF04650; YSIRK signal; 1.			
DR	PRINTS; PRO0015; GPOSANCHOR.			
DR	TIGRFAMS; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRFAMS; TIGR01168; YSIRK_anchor; 1.			
DR	PROSITE; PS50847; GRAM_POS_ANCHOR; Signal.			
RX	STRAIN=Serotype M55;			
RA	MEDLINE=95371690; PubMed=7643859; DOI=10.1016/0161-5890(95)00022-7;			
RA	Boyle M.D.P., Weber-Heymann J., Raeder R., Podbielski A.;			
RT	"Characterization of a gene coding for a type II bacterial IgG-binding protein".			
RT	Mol. Immunol. 32:665-678 (1995).			
CC	- - SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity).			
CC	an amide bond (By similarity).			
DR	EMBL; X72090; CAA5080.; -.			
DR	GO: 0016020; C membrane; IEA.			
DR	InterPro; IPR005877; Gpos_YSIRK.			
DR	InterPro; IPR001899; Gram_pos_anchor.			
DR	InterPro; IPR003345; M_repeat.			
DR	Pfam; PF00746; Gram_pos_anchor; 1.			
DR	Pfam; PF02370; M; 2.			
DR	PRINTS; PRO0015; GPOSANCHOR.			
DR	TIGRFAMS; TIGR01167; LPXTG_anchor; 1.			
DR	TIGRFAMS; TIGR01168; YSIRK_signal; 1.			
DR	PROSITE; PS50847; GRAM_POS_ANCHOR; 1.			
SQ	Cell wall; Peptidoglycan-anchor.			
SEQUENCE 550 AA; 61736 MW; 32294BFFF8805181B CRC64;				
Query Match Score 52.9%; Pred. No. 24; Length 550;				
Best Local Similarity 46.3%; Mismatches 3; Indels 13; Gaps 1;				
Matches 19; Conservative 3; Mismatches 6; Indels 13; Gaps 1;				
Qy 1 KQAEDK-----VKASREAKKQVEKALEQLEDKV 28				
Db 417 KVKEDKQISDASRKGRLRDASREAKKQVEKALEBANSKL 421				
RESULT 5				
Q54639	PRELIMINARY;	PRT; 100 AA.		
ID Q54639;				
AC	Q54639;	Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)			
DB	M1 Protein (Fragment).			
OS	Streptococcus pyogenes.			
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
Strptococcus.				
NCBI_TaxID=1314;				
OX [1]; RN				

RP SEQUENCE FROM N.A.
 RX MEDLINE=95172752; PubMed=7068273;
 RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
 RT "Genetic diversity and relationships among Streptococcus pyogenes
 strains expressing serotype M1 protein: recent intercontinental spread
 of a subclone causing episodes of invasive disease.";
 RT Infect. Immun. 63:994-1003(1995).
 DR EMBL; U20103; AAAB5116.1; -.
 DR HSSP; P13276; 1EQ1.
 DR GO:0016020; C:membrane; IEA.
 DR InterPro; IPR00345; M_repeat.
 DR PF02370; M: 1; -.
 DR P13276; 1EQ1.
 FT NON_TER 1 1
 FT 100 100
 SQ SEQUENCE 100 AA; 11243 MW; 9775831FA25DC463 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 100;
 Best Local Similarity 45.2%; Pred. No. 5.9;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Qy 5 DKYK-----ASREANKQVEKALEQLEDKV 28
 Db 28 DKVKEEKQISDASRQGLRDLDAASREANKQVEKALEEANSKL 69

RESULT 6
 ID Q54640 PRELIMINARY; PRT; 100 AA.
 AC Q54640;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE M1 protein (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95172752; PubMed=7068273;
 RA Musser J.M., Kapur V., Szeto J., Pan X., Swanson D.S., Martin D.R.;
 RT "Genetic diversity and relationships among Streptococcus pyogenes
 strains expressing serotype M1 protein: recent intercontinental spread
 of a subclone causing episodes of invasive disease.";
 RT Infect. Immun. 63:994-1003(1995).
 DR EMBL; U20104; AAAB5117.1; -.
 DR HSSP; P13276; 1EQ1.
 DR GO:0016020; C:membrane; IEA.
 DR InterPro; IPR00345; M_repeat.
 DR PF02370; M: 1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 100 AA; 11287 MW; 9773331914EDC2D3 CRC64;

Query Match 52.6%; Score 72; DB 2; Length 100;
 Best Local Similarity 45.2%; Pred. No. 5.9;
 Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;

Qy 5 DKYK-----ASREANKQVEKALEQLEDKV 28
 Db 28 DKVKEEKQISDASRQGLRDLDAASREANKQVEKALEEANSKL 69

RESULT 7
 ID Q9R3A1 PRELIMINARY; PRT; 100 AA.
 AC Q9R3A1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE M1 protein (Fragment).
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus. Pyogenes;
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3-3/317;
 RA Podbielski A.; Kauflund A.;
 RL Submitted (MAY-1992) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (BY SIMILARITY).
 DR EMBL; X66816; CAA4725.1; -.
 DR GO; GO:0005996; C:cell surface; IEA.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR PROSITE; PS50847; GRAM_pos_ANCHORING; 1.
 DR KW Cell wall; Peptidoglycan_anchor.
 DR InterPro; IPR01899; Gram_Pos_Anchor.
 DR InterPro; IPR00345; M_repeat.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF02370; M: 1.
 DR PRINTS; PR0015; GPOSANCHOR.
 DR DR

Query Match 52.6%; Score 72; DB 2; Length 198;

Best Local Similarity 45.2%; Pred. No. 11; Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;	DR GO:0005618; C:cell wall; IEA.
Qy 5 DVVK-----ASREAKQVEKALEFOLEDKV 28 Db 27 DVKEEKQISDASRQGLRDLDAASREAKQVEKALEBEANSKL 68	DR GO:0016020; C:membrane; IEA. DR InterPro; IPR001899; Gram_pos_anchor. DR InterPro; IPR003345; M_repeat. DR Pfam; PF00746; Gram_pos_anchor; 1. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPRTNG_anchor; 1. DR PROSITE; PS5084; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan-anchor. KW FT NON-TER 1 FT 208 AA; 226565 MW; 79972A9B7324729B CRC64;
RESULT 9 P95824 PRELIMINARY; PRT; 208 AA. ID P95824; AC P95824; RL 01-MAY-1997 (TREMBLrel. 03, Created) DT 01-MAR-1997 (TREMBLrel. 03, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) DB M protein (Fragment). OS Streptococcus Pyogenes. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OX NCBI_TaxID=1314; RN [1] RP SEQUENCE FROM N.A. RC STRAIN=M nontypeable group A; RA Brandt, E.R.; Good, M.P.; RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases. CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity). DR U65839; AAB40610.1; -. DR GO:000986; C:cell surface; IEA. DR GO:0005618; C:cell wall; IEA. DR GO:0016020; C:membrane; IEA. DR InterPro; IPR001899; Gram_pos_anchor. DR InterPro; IPR003245; M_repeat. DR Pfam; PF02370; M; 1. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;	DR GO:0005618; C:cell wall; IEA. DR GO:0016020; C:membrane; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
Query Match Best Local Similarity 45.2%; Pred. No. 11; Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
Qy 5 DVVK-----ASREAKQVEKALEFOLEDKV 28 Db 37 DVKEEKQISDASRQGLRDLDAASREAKQVEKALEBEANSKL 78	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
RESULT 10 P95826 PRELIMINARY; PRT; 208 AA. ID P95826; AC P95826; RL 01-MAY-1997 (TREMBLrel. 03, Created) DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update) DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update) DB M protein (Fragment). OS Streptococcus Pyogenes. OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; OC Streptococcus. OX NCBI_TaxID=1314; RP SEQUENCE FROM N.A. RC STRAIN=RH152-; RA Brandt, E.R.; Good, M.P.; RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases. CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by an amide bond (By similarity). DR U66605; AAB40612.1; -. GO:000986; C:cell surface; IEA.	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
Query Match Best Local Similarity 52.6%; Pred. No. 11; Matches 19; Conservative 2; Mismatches 3; Indels 18; Gaps 1;	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
Qy 5 DVVK-----ASREAKQVEKALEFOLEDKV 28 Db 37 DVKEEKQISDASRQGLRDLDAASREAKQVEKALEBEANSKL 211	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 208 AA; 22695 MW; 013FBBAB0A97FF42 CRC64;
RESULT 12 Q6V9Q3 PRELIMINARY; PRT; 251 AA. ID Q6V9Q3 AC Q6V9Q3 RL 05-JUL-2004 (TREMBLrel. 27, Created) DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update) DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 251 AA; 70727 MW; 470FF315DD4EB5F2 CRC64;	DR GO:0005618; C:cell wall; IEA. DR InterPro; IPR003345; M_repeat. DR Prints; PR00005; GPOSANCHOR. DR TIGRFAMS; TIGR01167; LPXTG_anchor; 1. DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1. DR Cell wall; Peptidoglycan_anchor. KW FT NON-TER 1 FT 251 AA; 70727 MW; 470FF315DD4EB5F2 CRC64;

OC Streptococcus,
NCBI_TaxID=1314;
RN [1] SEQUENCE FROM N.A.
RP Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
RC Moses A.B.; Hidalgo-Grass C.; Dan-Goor M.; Jaffe J.; Shzigovsky I.;
RA Ravins M.; Koreman Z.; Cohen-Poradosu R.; Nir-Paz R.;
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139420; C:membrane; IEA.
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
Pfam; PF02370; M; 1.
FT NON_TER 1 1
SQ SEQUENCE 251 AA; 251 MW; 2A66602AAA637D11 CRC64;
Query Match 52.6%; Score 72; DB 2; Length 251;
Best Local Similarity 45.2%; Pred. No. 13;
Matches 19; Conservative 2; Mismatches 3; Indels 18;
Gaps 1;
Qy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
Db 199 DKVKEEKQISDASRQGLRRLDLDAASREAKKQVEKALEEANSKL 245

RESULT 13
Q8GL87 PRELIMINARY; PRT; 279 AA.
AC Q8GL87;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB M_protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID=1314;
RN [1] SEQUENCE FROM N.A.
RP Dyall-Smith M.L.; Krejany S.; Srivakash K.S.; Delvecchio A.;
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139420; AAN64693.1;
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
Pfam; PF02370; M; 2.
FT NON_TER 1 1
SQ SEQUENCE 279 AA; 31224 MW; 16A600455BC5C3A0 CRC64;
Query Match 52.6%; Score 72; DB 2; Length 279;
Best Local Similarity 45.2%; Pred. No. 15;
Matches 19; Conservative 2; Mismatches 3; Indels 18;
Gaps 1;
Qy 5 DKVK-----ASREAKKQVEKALEQLEDKV 28
Db 202 DKVKEEKQISDASRQGLRRLDLDAASREAKKQVEKALEEANSKL 243

RESULT 14
Q8CLA6 PRELIMINARY; PRT; 282 AA.
AC Q8CLA6;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DB M_protein (Fragment).
GN Name=emm;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
NCBI_TaxID=1314;

RN [1] SEQUENCE FROM N.A.
RP Dyall-Smith M.L.; Krejany S.; Srivakash K.S.; Delvecchio A.;
RA McMillan D.;
RL Submitted (AUG-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY139409; AAN64682.1;
GO; GO:0016020; C:membrane; IEA.
InterPro; IPR003345; M_repeat.
Pfam; PF02370; M; 1.
FT NON_TER 1 1
SQ SEQUENCE 303 AA; 34562 MW; F76F37540B16CD1B CRC64;
Query Match 52.6%; Score 72; DB 2; Length 303;
Best Local Similarity 50.0%; Pred. No. 16;
Matches 18; Conservative 3; Mismatches 7; Indels 8;
Gaps 1;
Qy 1 KQABD-----KVKAASREAKKQVEKALEQLEDKV 28
Db 230 KVVSADASRQGLRRLDLDAASREAKKQVEKALEEANSKL 265

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